

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 06:11:13 ; Search time 6340.47 Seconds
(without alignments)
13027.239 Million cell updates/sec

Title: US-10-054-680-1
Perfect score: 2766
Sequence: 1 atggcgtgggttaaggttgca.....gctacatcaaggggttctaa 2766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
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13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match Length	DB	ID	
	1	2627.4	95.0	3186	11	BC036783 Homo sapi
	2	1786.4	64.6	1788	29	AY401283 Homo sapi
	3	1741.4	63.0	1788	29	AY401284 Pan trogl
	4	1624.4	58.7	2534	11	AK044636 Mus muscu
	5	1546.4	55.9	1788	29	AY401285 Mus muscu
	6	1258.2	45.5	4374	11	AK035163 Mus muscu
	7	1208.8	43.7	2922	29	AY398961 Homo sapi
	8	1169.8	42.3	2922	29	AY398963 Mus muscu
	9	1151.4	41.6	2516	29	AY408693 Homo sapi
	10	978.4	35.4	2881	29	AY398962 Pan trogl
	11	971	35.1	1589	11	CNSLT1IBJ BX248763 human ful
	12	948.4	34.3	3573	11	AK048160 Mus muscu
	13	899.6	32.5	941	13	BX374548 BX374548
	14	874.8	31.6	2515	29	AY408695 Mus muscu
	15	813.8	29.4	887	12	BI913344 603178823
	16	768.2	27.8	939	13	BX347210 BX347210
c	17	743.4	26.9	791	12	BI523145 603175911
	18	739.8	26.7	792	12	BI522813 603175911
	19	737.8	26.7	920	13	BX368185 BX368185
	20	708.4	25.6	922	13	BX390204 BX390204
	21	698.2	25.2	2472	29	AY408694 Pan trogl
	22	673.2	24.3	775	13	BQ770745 UI-M-FI0-
	23	657	23.8	665	13	BQ189572 UI-E-EJ1-
	24	605.4	21.9	704	14	CF729293 UI-M-HD0-
	25	598.6	21.6	971	13	BX368184 BX368184
	26	574.6	20.8	752	14	CF532853 UI-M-GH0-
	27	560.2	20.3	676	10	BB280958 BB280958
c	28	553.6	20.0	1062	29	CNS04DXR AL286344 Tetraodon
	29	516	18.7	527	12	BG910325 602805921
	30	503.8	18.2	588	14	CF533347 UI-M-FY0-
	31	483.2	17.5	854	13	BX325851 BX325851
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	33	452	16.3	717	13	BX501230 DKFZp779K
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	35	422.8	15.3	684	13	BU363818 603788721
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	37	412.4	14.9	503	28	BZ211245 CH230-426
	38	407.8	14.7	475	10	BF190598 237175 MA
c	39	407.4	14.7	499	28	BH349372 CH230-32M
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	41	397.2	14.4	911	13	BU901346 AGENCOURT
	42	390.2	14.1	597	13	BX502589 DKFZp779P
	43	376.8	13.6	694	13	BX854768 BX854768
	44	372.8	13.5	3063	11	BC023215 Homo sapi
	45	368.4	13.3	1201	13	BX355386 BX355386

ALIGNMENTS

RESULT 1

BC036783

LOCUS BC036783 3186 bp mRNA linear HTC 19-NOV-2003

DEFINITION Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3, mRNA (cDNA clone IMAGE:5732743), with apparent retained intron.

ACCESSION BC036783

VERSION BC036783.1 GI:23331089

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3186)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 3186)

AUTHORS

Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (23-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nhgri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 79 Row: j Column: 21

This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 17865803

This clone has the following problem: retained intron.

FEATURES	Location/Qualifiers
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	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:5732743"
	/tissue_type="Brain, hippocampus"
	/clone_lib="NIH_MGC_124"
	/lab_host="DH10B"
	/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 95.0%; Score 2627.4; DB 11; Length 3186;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2628; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	558	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	617
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	618	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	677
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	678	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	737
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	738	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAG	797
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	798	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	857
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	858	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	917

Qy	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1038	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1097
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Db	1338	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1397
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
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Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1458	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1517
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Db	1638	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1697
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Db	1698	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1757

Qy	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1758	GACCCATGTTCTTACCAAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1817
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
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Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
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Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1938	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1997
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Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
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Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
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Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
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Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC	2100

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Db      2598 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC 2657
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Db      3138 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAA 3186

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RESULT 2

AY401283

LOCUS AY401283 1788 bp DNA linear GSS 15-DEC-2003

DEFINITION Homo sapiens SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY401283

VERSION AY401283.1 GI:39757272

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1788)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers
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ORIGIN

Query Match 64.6%; Score 1786.4; DB 29; Length 1788;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
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Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
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Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
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Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
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Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320

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Db 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAA 1788
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Db 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGTAA 1788

RESULT 3

AY401284

LOCUS AY401284 1788 bp DNA linear GSS 15-DEC-2003

DEFINITION Pan troglodytes SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY401284

VERSION AY401284.1 GI:39757273

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1788)

AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Db	61 TTTGTGCTCTTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2534)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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ORIGIN

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Query Match      58.7%; Score 1624.4; DB 11; Length 2534;
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Matches 1740; Conservative 0; Mismatches 156; Indels 2; Gaps 2;

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Db 1863 GGAAAGGGGGAGATATATCCAAGACCATGTACGTGGACTACAAAACAGAGGACGGCTCCG 1922

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RESULT 5

AY401285

LOCUS AY401285 1788 bp DNA linear GSS 15-DEC-2003

DEFINITION Mus musculus SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION AY401285

VERSION AY401285.1 GI:39757274
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1788)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1788)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 gene <1. .>1788
 /gene="SLC8A3"
 /locus_tag="HCM0839"

ORIGIN

Query Match 55.9%; Score 1546.4; DB 29; Length 1788;
 Best Local Similarity 91.6%; Pred. No. 0;
 Matches 1637; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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 Db 1 ATGGCGTGGTTACGGCTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACT 60
 Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861

REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4374)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
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putative"

ORIGIN

Query Match 45.5%; Score 1258.2; DB 11; Length 4374;
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Matches 1829; Conservative 0; Mismatches 783; Indels 51; Gaps 5;

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Qy	2683	ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC	2742
Db	2963	ACCACCGCTCTCTTCCTGGGCCTCTGGTTCCTCTACATTCTCTCTCCAGCCTGGAGGCT	3022
Qy	2743	TATTGCTACATCAAGGGGTTCTA	2765
Db	3023	TACTGCCACATCCGGGGCTTCTA	3045

RESULT 7

AY398961

LOCUS AY398961 2922 bp DNA linear GSS 15-DEC-2003

DEFINITION Homo sapiens SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY398961

VERSION AY398961.1 GI:39754950

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2922)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

REFERENCE 2 (bases 1 to 2922)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

	Location/Qualifiers
source	1..2922 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
gene	<1..>2922 /gene="SLC8A1" /locus_tag="HCM0065"

ORIGIN

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Query Match      43.7%;   Score 1208.8;   DB 29;   Length 2922;
Best Local Similarity 66.9%;   Pred. No. 6e-286;
Matches 1887;   Conservative    0; Mismatches 762; Indels 171; Gaps 5;
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Qy	109	GACGTGCCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGT CATCGGACTGCAAGGAG	168
Db	112	GAAATGGAAGGAGAAGGAAATGAACTGGTG AATGTACTGGATCATATTACTGTAAGAAA	171
Qy	169	GGTGTGCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCCTTGGGGACAAGATTGCCAGG	228
Db	172	GGGGTGATTTTGCCCCATTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAAATTGCTAGA	231
Qy	229	GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCAT TGCTGAC	288
Db	232	GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT	291
Qy	289	CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA	348
Db	292	CGGTTTCATGT CCTCTATAGAAGTCATCACATCTCAAGAAAAAGAAATAACCATAAAGAAA	351
Qy	349	CCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAACTGTCTCCAACCTG	408
Db	352	CCAATGGAGAGACCACCAAGACAAC TGTGAGGATCTGGAATGAAACAGTTTCTAACCTG	411
Qy	409	ACCCTTATGGCCCTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT	468

Db 412 ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTTCAGTAATTGAAGTGTGT 471
 Qy 469 GGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC 528
 Db 472 GGCCATAACTTCACTGCAGGAGACCTCGGTCTAGCACCATCGTGGGAAGTGTGCATTTC 531
 Qy 529 AACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG 588
 Db 532 AATATGTTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG 591
 Qy 589 ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG 648
 Db 592 ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG 651
 Qy 649 CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC 708
 Db 652 CTTTACATTATTTTGTCTGTCATATCTCCTGGTGTGTGGAGGTCTGGGAAGGTTTGCTT 711
 Qy 709 ACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC 768
 Db 712 ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTTCGCTTGGGTAGCGGATAGGAGACTTCTG 771
 Qy 769 TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG 828
 Db 772 TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA 831
 Qy 829 ACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATGAAT 879
 Db 832 CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT 891
 Qy 880 TCCCATTTTCTAGATGGGAACCTGGTGGCCCTGGAAGGGAAG----- 921
 Db 892 TCTCATGTTGAAAATTTCTTAGATGGTGTCTGTTTCTGGAGGTGGATGAGAGGGACCAA 951
 Qy 922 GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC 981
 Db 952 GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACCTAAGCAGAAGCAT 1011
 Qy 982 CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAA 1041
 Db 1012 CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG 1071
 Qy 1042 CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT 1101
 Db 1072 CAAAAAAGTAGAGCATTTTATCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC 1131
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 Db 1132 ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCAGCATGCACGAGGTCAAC 1191
 Qy 1162 ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG 1218
 Db 1192 ACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1251
 Qy 1219 TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGGAGAAAGGGGGAGACATGTCA 1278

Db	1252	TGTCCTGGAGAACTGTGGTACTGTGGCCCTTACCATTTATCCGCAGAGGTGGTGATTGACT	1311
Qy	1279	AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT	1338
Db	1312	AACACTGTGTTTGTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT	1371
Qy	1339	GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG	1398
Db	1372	GAATTTACTGAAGGAAGTGTGGTGTTTAAGCCTGGTGATACCAGAAGGAAATCAGAGTG	1431
Qy	1399	GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT	1458
Db	1432	GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTTCTTGTCATCTCAGCAAT	1491
Qy	1459	GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCCTCAGCAATATTCAACAGTCTT	1518
Db	1492	GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC-----CAATCAT	1542
Qy	1519	CCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGAT	1578
Db	1543	GTTTCTACACTTGCCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACATATTTTGTATGAT	1602
Qy	1579	GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGT	1638
Db	1603	GACCACGCAGGCATTTTACTTTTGAAGAACCTGTGACTCATGTGAGTGAGAGCATTTGGC	1662
Qy	1639	GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCCTT	1698
Db	1663	ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT	1722
Qy	1699	AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAG	1758
Db	1723	AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTTGAGGACACTTGTGGAGAG	1782
Qy	1759	TTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAG	1818
Db	1783	CTCGAATTCCAGAATGATGAAATTGTCAAACAATATCAGTCAAGGTAATTGATGATGAG	1842
Qy	1819	GAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAA---	1875
Db	1843	GAGTATGAGAAAAACAAGACCTTCTTCCTTGAGATTGGAGAGCCCCGCCTGGTGGAGATG	1902
Qy	1876	-----	1875
Db	1903	AGTGAGAAGAAAGNNN	1962
Qy	1876	-----	1875
Db	1963	NNNNNNNGCCAACCTGTCTTCAGGAAGGTTTCATGCTAGAGAACATCCGATTCTCTCTACT	2022
Qy	1876	-----CGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAG	1926
Db	2023	GTAATCACCATTGCAGACGAATATGATGACAAGCAGCCACTGACCAGCAAAGAGGAAGAG	2082
Qy	1927	GCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAAGTAGAAGTC	1986
Db	2083	GAGAGGCGCATTCAGAAATGGGGCGCCCCATCCTGGGAGAGCACACCAAGTTGGAAGTG	2142

Qy	1987	ATCATTGAAGAGTCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAAC	2046
Db	2143	ATCATTGAAGAATCCTATGAATTCAAGAGTACTGTGGACAAACTCATTAAGAAGACAAAC	2202
Qy	2047	CTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTCATGGAGGCCATCACCGTC	2106
Db	2203	CTGGCCTTGTGGTTGGGACTAACAGCTGGAGAGAACAGTTCATTGAAGCTATCACTGTC	2262
Qy	2107	AGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTT	2166
Db	2263	AGTGCTGGGGAAGATGATGACGACGATGAATGTGGGGAAGAGAAGCTGCCCTCCTGTTTC	2322
Qy	2167	GACTACGTCATGCACTTCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCC	2226
Db	2323	GATTACGTGATGCACTTTCTGACTGTGTTCTGGAAGGTCCTGTTTGCCTTCGTCCCCCT	2382
Qy	2227	ACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTC	2286
Db	2383	ACTGAATACTGGAATGGCTGGGCGTGTTTCATTGTCTCCATCCTCATGATTGGCCTACTG	2442
Qy	2287	ACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCA	2346
Db	2443	ACAGCTTTCATTGGAGACCTGGCTTCCCACTTTGGCTGCACCATTGGCCTGAAAGATTCT	2502
Qy	2347	GTCACAGCTGTTGTTTTCTGTTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCCAGCAA	2406
Db	2503	GTGACTGCAGTCGTGTTCTGTCGCACTTGGAAACATCAGTGCCAGACACATTGTCAGCAA	2562
Qy	2407	GCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAAC	2466
Db	2563	GTGGCAGCCACCCAGGACCAGTATGCAGACGCCTCCATAGGTAACGTACGGGCAGCAAC	2622
Qy	2467	GCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCT	2526
Db	2623	GCGGTGAATGTCTTCTGGGAATCGGTGTGGCCTGGTCCATCGCTGCCATCTACCACGCA	2682
Qy	2527	CTGCAGGGACAGGAGTTCCACGTGTGGCCGGCACACTGGCCTTCTCCGTCAACCTCTTC	2586
Db	2683	GCCAATGGGGAACAGTTCAAAGTGTCCCCTGGCACACTAGCTTCTCTGTCACTCTCTTC	2742
Qy	2587	ACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGCCGCACCTGGGA	2646
Db	2743	ACCATTTTGTCTTTCATCAATGTGGGGGTGCTGCTGTATCGGCGGAGGCCAGAAATCGGA	2802
Qy	2647	GGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTG	2706
Db	2803	GGTGAGCTGGGTGGGCCCCGGACTGCCAAGCTCCTCACATCCTGCCTCTTTGTGCTCCTA	2862
Qy	2707	TGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTCTAA	2766
Db	2863	TGGCTCTTGTACATTTTCTTCTCCTCCCTGGAGGCCTACTGCCACATAAAGGCTTCTAA	2922

RESULT 8

AY398963

LOCUS

AY398963

2922 bp

DNA

linear

GSS 15-DEC-2003

DEFINITION Mus musculus SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY398963

VERSION AY398963.1 GI:39754952

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2922)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2922)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES Location/Qualifiers

source 1..2922
/organism="Mus musculus"
/mol_type="genomic DNA"
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gene <1..>2922
/gene="SLC8A1"
/locus_tag="HCM0065"

ORIGIN

Query Match 42.3%; Score 1169.8; DB 29; Length 2922;
Best Local Similarity 66.2%; Pred. No. 2.4e-276;
Matches 1845; Conservative 0; Mismatches 771; Indels 171; Gaps 5;

Qy	142	TGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTGCCAATCTGGTACCCGGAGAAC	201
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Qy	202	CCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATG	261
Db	205	CCATCTTTTGGGGACAAAATTGCTAGAGCAACTGTGTATTTTGTGGCCATGGTCTACATG	264
Qy	262	TTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCT	321
Db	265	TTCCTTGGAGTTTCTATTATTGCAGACCGGTTTATGTCCTCTATAGAGGTCATCACCTCT	324
Qy	322	CAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACACCCTATTCGG	381
Db	325	CAAGAGAAAGAAATAACGATAAAGAAACCGAATGGAGAGACCACCAAGACGACGGTGAGA	384

Qy 382 GTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAG 441
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 Db 385 ATCTGGAACGAGACTGTGTGGAACCTGACCTTGATGGCCCTGGGATCTTCTGCTCCTGAG 444

Qy 442 ATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCT 501
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 Db 445 ATTCTCCTGTGAGTCATTGAAGTGTGCGGCCATAACTTCACCGCAGGGGACCTGGGTCCC 504

Qy 502 TCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTAC 561
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 Db 505 AGCACCATCGTGGGAAGTGTGCCTTTAACATGTTTCATCATAATCGCACTCTGTGTTTAC 564

Qy 562 GTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCT 621
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 Db 565 GTGGTCCCTGATGGAGAGACAAGGAAGATCAAGCATCTGCGTGTGTTCTTTGTGACAGCA 624

Qy 622 GCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGT 681
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 Db 625 GCCTGGAGCATCTTTGCCTATACCTGGCTTTATATAATCTTGTCTGTGAGCTCTCCTGGA 684

Qy 682 GTGGTCCAGGTTTGGGAAGGCCTCTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTG 741
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 Db 685 GTTGTGGAGGTCTGGGAAGGCTTGCTTACTTTCTTCTTCTTTCCCATCTGCGTTGTGTTT 744

Qy 742 GCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAGTACCGCACA 801
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 Db 745 GCGTGGGTAGCAGACAGGCGGCTTCTCTTTTACAAGTATGTCTACAAGCGGTACAGGGCC 804

Qy 802 GACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCC-----TAAGGGC 852
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 Db 805 GGCAAGCAGAGGGGGATGATCATTGAACATGAAGGAGACAGACCAGCTTCCAAAAGTGA 864

Qy 853 ATTGAGATGGATGGGAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTG 912
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 Db 865 ATCGAAATGGATGGGAAAGTGGTCAACTCTCATGTTGACAATTTCTTAGATGGGGCTCTG 924

Qy 913 GAAGGG-----AAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGG 954
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 Db 925 GTTTTGAAGTTGATGAGAGGGACCAAGATGATGAGGAAGCCAGGCGTGAGATGGCAAGG 984

Qy 955 ATTCTCAAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATG 1014
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Qy 1015 GCCAATTACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCC 1074
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 Db 1045 GCCAACTACCAGGTCCTAAGTCAACAGCAGAAAAGCCGAGCATTTTACAGGATTCAAGCT 1104

Qy 1075 ACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACCAAGCAAG 1134
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 Db 1105 ACTCGCCTGATGACCGGAGCTGGCAACATCTTGAAGAGGCACGCAGCTGATCAAGCAAGG 1164

Qy 1135 AAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCCTG---AGGACTTTATTTCCAAG 1191
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 Db 1165 AAGGCTGTGAGTATGCATGAAGTCAACATGGAAATGGCTGAAAACGACCCAGTCAGTAAG 1224

Qy	1192	GTCTTCTTTTGACCCATGTTCTTTACCAAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACA	1251
Db	1225	ATCTTCTTTTGAGCAAGGAACATACCAGTGTCTAGAGAAGTGTGGTACTGTGGCCCTCACC	1284
Qy	1252	GTGGTGAGGAAAGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGAT	1311
Db	1285	ATTATGCGCAGAGGGGGCGACTTGAGCACCACGTGTGTTTGTTGACTTCAGGACAGAAGAC	1344
Qy	1312	GGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCCTGAAGCCA	1371
Db	1345	GGCACAGCCAATGCTGGGTCTGATTATGAATTCACGGAAGGGACTGTGATCTTCAAACCA	1404
Qy	1372	GGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGAT	1431
Db	1405	GGGGAGACCCAGAAGGAAATCAGAGTTGGCATCATTGATGATGATATCTTTGAAGAAGAT	1464
Qy	1432	GAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGG	1491
Db	1465	GAAAACTTCCTTGTCATCTTAGCAATGTCAGAGTCTCTTCAGATGTTTCAGAAGATGGC	1524
Qy	1492	ATGCCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGT	1551
Db	1525	AT-----ACTAGAATCCAATCACGCTTCTTCAATTGCTTGTCTTGGGTCACCCAGC	1575
Qy	1552	GTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGAT	1611
Db	1576	ACTGCCACCATAACCATTTTTGATGATGACCATGCAGGCATCTTACATTTGAGGAACCC	1635
Qy	1612	ACTATTCAATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGT	1671
Db	1636	GTGACTCACGTGAGCGAGAGCATTTGGCATCATGGAGGTGAAGGTTTGTGAGAACCTCTGGA	1695
Qy	1672	GCCCGGGGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGT	1731
Db	1696	GCTCGAGGAAATGTTATCATTCCTTACAAAACATTGTAAGGCACAGCCCAGGTGGAGGG	1755
Qy	1732	GAGGACTTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACC	1791
Db	1756	GAAGACTTTGAGGACACCTGTGGAGAGCTCGAATTCAGAACGATGAAATAGTCAAAACA	1815
Qy	1792	ATAAGGGTTAAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCC	1851
Db	1816	ATATCAGTCAAGGTAATCGATGACGAGGAGTATGAGAAAAACAAGACCTTCTTCATTGAG	1875
Qy	1852	CTTGGTGAACCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAG-----	1905
Db	1876	ATTGGAGAGCCCCGTCTGGTGGAGATGAGTGAGAAGAAAGNNNNNNNNNNNNNNNNNNNN	1935
Qy	1906	-----	1905
Db	1936	NNNGCCAACCTATCTTCAGGAAGGTCCAT	1995
Qy	1906	-----	1905
Db	1996	GCTAGAGATCATCCGATTCCCTCTACTGTAATCACCATCTCAGAGGAATATGATGACAAG	2055
Qy	1906	-----CTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTA	1959

Db	2056	CAGCCACTGACCAGCAAAGAAGAGGAGGAGAGGCGCATTGCGGAAATGGGGCGCCCCATC	2115
Qy	1960	TTGGGTGAACACCCCAAAGTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACG	2019
Db	2116	CTAGGCGAGCACACCAAGCTGGAGGTGATCATCGAAGAGTCTTACGAATTCAAGAGCACT	2175
Qy	2020	GTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGG	2079
Db	2176	GTGGACAAACTCATTAAGAAGACGAACCTGGCCCTTGTGGTGGGGACCAACAGCTGGAGA	2235
Qy	2080	GACCAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCC	2139
Db	2236	GAGCAGTTTATCGAAGCCATCACTGTCAGCGCTGGGAAGATGACGATGATGATGAATGT	2295
Qy	2140	GGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTGATGCACCTTCTGACTGTCTTCTGG	2199
Db	2296	GGGGAGGAGAAGCTGCCCTCCTGTTTTGATTACGTGATGCACCTTCTCACAGTGTTCTGG	2355
Qy	2200	AAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCC	2259
Db	2356	AAGGTTCTGTTTGCCTTCGTCCCACCTACAGAATACTGGAATGGCTGGGCCTGCTTCATT	2415
Qy	2260	GTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTC	2319
Db	2416	GTCTCCATCCTCATGATCGGCCTACTGACCGCCTTCATTGGAGACCTGGCTTCCCACTTT	2475
Qy	2320	GGCTGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCTGGCATTGGGCACC	2379
Db	2476	GGCTGCACCATTGGTCTGAAAGATTCCGTGACTGCCGTTGTGTTTGTGCTCTTGGAACC	2535
Qy	2380	TCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCC	2439
Db	2536	TCGGTGCCAGACACATTTGCCAGCAAAGTAGCAGCTACCCAGGACCAGTATGCAGATGCG	2595
Qy	2440	TCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCC	2499
Db	2596	TCTATAGGCAATGTCACTGGAAGCAATGCTGTGAATGTCTTCCTGGGAATCGGCGTGGCC	2655
Qy	2500	TGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTGGCCGGC	2559
Db	2656	TGGTCCATTGCTGCCATCTACCATGCGGCAACGGGAACAGTTCAAAGTGTCCTCCGGC	2715
Qy	2560	AACTGGCCTTCTCCGTCAACCTCTTACCATCTTTGCATTTGTCTGCATCAGCGTGCTC	2619
Db	2716	ACGCTAGCTTTCTCTGTCACTCTCTTCACTATTTTGTCTTTCATCAACGTGGGGGTGCTG	2775
Qy	2620	TTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTC	2679
Db	2776	CTGTATCGGCGGAGGCCAGAAATAGGAGGTGAGCTGGGAGGGCCCCGACTGCCAAGCTC	2835
Qy	2680	GCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAG	2739
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Qy	2740	GCCTATTGCTACATCAAGGGGTTCTAA	2766

Db 2896 GCCTACTGCCACATAAAGGGCTTCTAA 2922

RESULT 9

AY408693

LOCUS AY408693 2516 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM3309 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY408693

VERSION AY408693.1 GI:39764664

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2516)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2516)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers
source 1. .2516
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1..>2516
/locus_tag="HCM3309"

ORIGIN

Query Match 41.6%; Score 1151.4; DB 29; Length 2516;
Best Local Similarity 66.0%; Pred. No. 7.6e-272;
Matches 1673; Conservative 0; Mismatches 809; Indels 51; Gaps 5;

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Qy 266 TTGGGGTGTCCATCATTTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 325
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Db 1 TGGGAGTGTCCATCATCGCCGACCGTTTCATGGCGGCCATCGAGGTCATCACGTCAAAG 60

Qy 326 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACTATTTCGGGTCT 385
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Db 61 AGAAGGAGATCACCATCACCAAGGCCAACGGTGAGACCAGCGTGGGCACCGTTCGCATCT 120

Qy 386 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATAC 445
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Db 121 GGAATGAGACGGTGTCCAACCTCACGCTCATGGCCCTGGGCTCCTCCGCACCTGAGATCC 180

Qy 446 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTA 505
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Db 181 TGCTGTCACTCATCGAAGTCTGCGGCCACAACCTCCAGGCGGGTGAGCTGGGCCCAGGCA 240

Qy 506 CCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGA 565
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Db 241 CCATCGTGGGCAGCGCTGCCTTCAACATGTTTGTGGTCATCGCCGTGTGCATCTACGTCA 300

Qy 566 TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTT 625
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Db 301 TCCCAGCCGGCGAGAGCCGCAAGATCAAGCACCTGAGAGTCTTCTTTGTCACTGCCTCTT 360

Qy 626 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 685
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Db 361 GGAGCATCTTCGCCTATGTCTGGCTTTATCTCATCCTTGCTGTTTTTTCCCCCGGTGTGG 420

Qy 686 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCT 745
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Qy 746 GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 805
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Db 481 GGATGGCCGACAAGCGGCTGCTCTTCTACAAGTACGTGTACAAGCGCTACCGCACCGACC 540

Qy 806 AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG 865
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Db 541 CACGCAGCGGCATCATCATAGGCGCCGAGGGCGACCCCGAAGAGCATCGAGCTGGACG 600

Qy 866 GGAAAATGATGAATTCCCATTTTCTAGATGGGAA-----CCTGGTGCCCTGG 913
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Db 601 GCACGTTTCGTGGGCGCCGAGGCCCCAGGTGAGCTGGGCGGCCTGGGCCCCGGGCCCGCCG 660

Qy 914 AAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGC 973
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Db 661 AGGCGCGCGAGCTGGACGCCAGCCGCCGCGAGGTATCCAGATCCTCAAGGACCTCAAGC 720

Qy 974 AAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTT 1033
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Qy 1034 CCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTG 1093
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Db 841 CCGGGAACGTGCTGCGCAGACACGCGGCGGACGCCTCGCGCAGGGCGGC---GCCGGCCG 897

Qy 1154 AGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTT 1213
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Db 898 AGGGCGCGGGCGAGGACGAAGACGACGGCGCCAGCCGCATCTTCTTCGAGCCTAGCCTCT 957

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Qy 2096 CCATCACCGTCAGTGCA---GCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGC 2152
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Qy 2153 TGCCCTCCTGCTTTGACTACGTACGTGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTG 2212
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Qy 2513 CCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCT 2572
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Qy 2633 GGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGC 2692
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 Db 2383 GGCCGCACATCGGCGGCGAGCTGGGCGGCCCGCGCGGACCCAAGCTCGCCACCACCGCGC 2442

Qy 2693 TCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACA 2752
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 Db 2503 TCCGGGGCTTCTA 2515

RESULT 10

AY398962

LOCUS AY398962 2881 bp DNA linear GSS 15-DEC-2003

DEFINITION Pan troglodytes SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY398962

VERSION AY398962.1 GI:39754951

KEYWORDS GSS.

Qy	409	ACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT	468
Db	376	NNN	435
Qy	469	GGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC 	528
Db	436	NNCCATCGTGGGAAGTGCTGCATTTC	495
Qy	529	AACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG 	588
Db	496	AATATGTTTCATCATTATTGCACTCTGTGTTTTATGTGGTCCCTGACGGAGAGACAAGGAAG	555
Qy	589	ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCCTACATCTGG 	648
Db	556	ATTAAGCATTTGCGTGTGTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCCTACACCTGG	615
Qy	649	CTCTATATGATTCTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTC 	708
Db	616	CTTTACATTATTTTGTCTGTCATATCTCCTGGTGTGTGGAGGTCTGGGAAGGTTTGCTT	675
Qy	709	ACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC 	768
Db	676	ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTTCGCTTGGGTAGCGGATAGGAGACTTCTG	735
Qy	769	TTCTACAAATACATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG 	828
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Db	796	CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT	855
Qy	880	TCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAG----- 	921
Db	856	TCTCATGTTGAAAATTTCTTAGATGGTGCTCTGGTTCTGGAGGTGGATGAGAGGGACCAA	915
Qy	922	GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC 	981
Db	916	GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACCTTAAGCAGAAGCAT	975
Qy	982	CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAA 	1041
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Qy	1042	CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT 	1101
Db	1036	CAAAAAAGTAGAGCATTTTATCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC	1095
Qy	1102	ATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC 	1161
Db	1096	ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCAGCATGCACGAGGTCAAC	1155
Qy	1162	ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG 	1218
Db	1156	ACTGAAGTGACTGAAAATGACCCTGTTAGTAAGATCTTCTTTGAACAAGGGACATATCAG	1215
Qy	1219	TGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCA	1278

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Qy	1279	AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT	1338
Db	1276	AACACTGTGTTTGTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT	1335
Qy	1339	GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG	1398
Db	1336	GAATTTACTGAAGGAAGTGTGGTGTAAAGCCTGGTGAGACCCAGAAGGAAATCAGAGTG	1395
Qy	1399	GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT	1458
Db	1396	GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTTCTTGTGCATCTCAGCAAT	1455
Qy	1459	GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT	1518
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Qy	1519	CCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGAT	1578
Db	1507	GTTTCTACACTTGCTTGCCTCGGATCTCCCNNACTGCCACTGTAAGTATTTTTGATGAT	1566
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Db	1567	GACCACGCAGGCATTTTACTTTTGAAGAACCTGTGACTCATGTGAGTGAGAGCATTGGC	1626
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Qy	1819	GAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGT	1878
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Db	1867	NN	1926
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Qy	1906	-----CTGACTATGGAAGAAGAGGAG	1926
Db	1987	GTAATCACCATTGCAGNNGAATATGATGACAAGCAGCCACTGACCAGCAAAGAGGAAGAG	2046
Qy	1927	GCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAAGTAGAAGTC	1986

Db 2047 GAGAGGCGCATTGCAGAAATGGGGCGCCCCATCCTGGGAGAGCACACCAAGTTGGAAGTG 2106
 Qy 1987 ATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAAC 2046
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 Db 2227 AGTGCTGGGGAAGATGATGACGACGATGAATGTGGGGAAGAGAAGCTGCCCTCCTGTTTC 2286
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 Db 2527 GTGGCAGCCACCCAGGACAGTATGCAGACGCCTCCATAGGTAACGTACGGGCAGCAAC 2586
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 Qy 2647 GGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTG 2706
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 Db 2767 GGTNNNNNGGTNGGCCCCGGACTGCCAAGCTCCTCACATNCTGCCTCTTTGTGCTCCTA 2826
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 Db 2827 TGGCTCTTGACATTTTCTTCTCCTCCNTGGAGGCCTACTGCCACATAAAAGGCT 2881

LOCUS CNSLT1IBJ 1589 bp mRNA linear HTC 18-JUN-2003
 DEFINITION human full-length cDNA 5-PRIME end of clone CS0DB006YD18 of Neuroblastoma of Homo sapiens (human).
 ACCESSION BX248763
 VERSION BX248763.1 GI:28375580
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1589)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
 REFERENCE 2 (bases 1 to 1589)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (13-FEB-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
 FEATURES
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 ORIGIN

Query Match 35.1%; Score 971; DB 11; Length 1589;
 Best Local Similarity 100.0%; Pred. No. 1.6e-227;
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 Db 619 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 678

Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	679	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	738
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	739	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	798
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	799	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	858
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	859	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	918
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	919	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	978
Qy	361	ACCAGCACAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	979	ACCAGCACAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	1038
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	1039	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	1098
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1099	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1158
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1159	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1218
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1219	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1278
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1279	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1338
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1339	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1398
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1399	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1458
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1459	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1518
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960

Db 1519 CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1578
 Qy 961 AAGGATCTGAA 971
 Db 1579 AAGGATCTGAA 1589

RESULT 12

AK048160

LOCUS AK048160 3573 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130038C08 product:solute carrier family 8 (sodium/calcium exchanger), member 1, full insert sequence.

ACCESSION AK048160

VERSION AK048160.1 GI:26339181

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE

4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE

5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3573)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES

source Location/Qualifiers

1. .3573

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM_DB:C130038C08"

/db_xref="MGI:2414212"

/db_xref="taxon:10090"

/clone="C130038C08"

/tissue_type="head"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="16 days embryo"

CDS

<1. .2122

/note="unnamed protein product; putative solute carrier family 8 (sodium/calcium exchanger), member 1 (MGD|MGI:107956, GB|NM_011406, evidence: BLASTN, 99%, match=1583)"

/codon_start=2

/protein_id="BAC33262.1"

/db_xref="GI:26339182"

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TEDGTANAGSDYEFTEGTVIFKPGETQKEIRVGIIDDDIFEEDENFLVHLSNVRVSSD
VSEDGILESNHASSIACLGSSSTATITIFDDDHAGIFTFEFPVTHVSESIGIMEVKVL
RTSGARGNVIIPYKTIEGTARGGGEDFEDTCGELEFQNDIEVKTISVKVIDDEEYEKN
KTFEIEIGEPRLVEMSEKKGGFTLTEEYDDKQPLTSKEEEEERRIAEMGRPILGEHTKL
EVIIIEESYEFKSTVDKLIKKTNLALVGTNSWREQFIEAITVSAGEDDDDDDECGEKLL
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IGLKDSVTAVVFVALGTSVPGPTL"

Query Match 34.3%; Score 948.4; DB 11; Length 3573;
Best Local Similarity 67.8%; Pred. No. 9.6e-222;
Matches 1434; Conservative 0; Mismatches 616; Indels 66; Gaps 5;

Qy	964	GATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTAC	1023
Db	662	GAACCTAAGCAGAAGCATCCTGAGAAAGAAATTGAGCAATTAATAGAATTAGCCAACCTAC	721
Qy	1024	TATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATG	1083
Db	722	CAGGTCCTAAGTCAACAGCAGAAAAGCCGAGCATTTTACAGGATTCAAGCTACTCGCCTG	781
Qy	1084	ATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACCAAGCCAAGAAGGCCTCC	1143
Db	782	ATGACCGGAGCTGGCAACATCTTGAAGAGGCACGCAGCTGATCAAGCAAGGAAGGCTGTC	841
Qy	1144	AGCATGAGCGAGGTGCACACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	842	AGTATGCATGAAGTCAACATGGAAATGGCTGAAAACGACCCAGTCAGTAAGATCTTCTTT	901
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	902	GAGCAAGGAACATACCAGTGTCTAGAGAACTGTGGTACTGTGGCCCTCACCATTATGCGC	961
Qy	1261	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	962	AGAGGGGGGCGACTTGAGCACCCTGTGTTTGTGACTTCAGGACAGAAGACGGCACAGCC	1021
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1022	AATGCTGGGTCTGATTATGAATTCACGGAAGGGACTGTGATCTTCAAACCAGGGGAGACC	1081
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1082	CAGAAGGAAATCAGAGTTGGCATCATTGATGATGATATCTTTGAAGAAGATGAAAACCTTC	1141
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCCTCCA	1500
Db	1142	CTTGTGCATCTTAGCAATGTCAGAGTCTCTTCAGATGTTTCAGAAGATGGCATACTAGAA	1201
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1202	TC-----CAATCACGCTTCTTCAATTGCTTGTCTTGGGTCTCCAGCACTGCCACC	1252
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1253	ATAACCATTTTTGATGATGACCATGCAGGCATCTTTACATTTGAGGAACCCGTGACTCAC	1312
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1313	GTGAGCGAGAGCATTTGGCATCATGGAGGTGAAGGTTTTGAGAACCCTCTGGAGCTCGAGGA	1372
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1373	AATGTTATCATTTCCCTACAAACTATTGAAGGCACAGCCGAGGTGGAGGGGAAGACTTT	1432
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1433	GAGGACACCTGTGGAGAGCTCGAATTCCAGAACGATGAAATAGTCAAACAATATCAGTC	1492
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860

Db	1493	AAGGTAATCGATGACGAGGAGTATGAGAAAAACAAGACCTTCTTCATTGAGATTGGAGAG	1552
Qy	1861	CCGAAATGGATGGA-----ACGTGGAATATCAGATGTG	1893
Db	1553	CCCCGTCTGGTGGAGATGAGTGAGAAGAAAGGTGGCTTACATTAACAGAGGAATATGAT	1612
Qy	1894	ACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAG	1953
Db	1613	GACAAGCAGCCACTGACCAGCAAAGAAGAGGAGGAGAGGCGCATTGCGGAAATGGGGCGC	1672
Qy	1954	CCAGTATTGGGTGAACACCCCAAAGTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAG	2013
Db	1673	CCCATCCTAGGCGAGCACACCAAGCTGGAGGTGATCATCGAAGAGTCTTACGAATTCAAG	1732
Qy	2014	ACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCC	2073
Db	1733	AGCACTGTGGACAAACTCATTAAGAAGACGAACCTGGCCCTTGTGGTGGGGACCAACAGC	1792
Qy	2074	TGGAGGGACCAAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGAT	2133
Db	1793	TGGAGAGAGCAGTTTATCGAAGCCATCACTGTCAGCGCTGGGGAAGATGACGATGATGAT	1852
Qy	2134	GAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTC	2193
Db	1853	GAATGTGGGGAGGAGAAGCTGCCCTCCTGTTTTGATTACGTGATGCACTTCTCACAGTG	1912
Qy	2194	TTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGC	2253
Db	1913	TTCTGGAAGGTTCCTGTTTGCCTTCGTCCACCTACAGAATACTGGAATGGCTGGGCCTGC	1972
Qy	2254	TTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCG	2313
Db	1973	TTCATTGTCTCCATCCTCATGATCGGCCTACTGACCGCCTTCATTGGAGACCTGGCTTCC	2032
Qy	2314	CACTTCGGCTGCACCATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTCGTGGCATT	2373
Db	2033	CACTTTGGCTGCACCATTGGTCTGAAAGATTCCGTGACTGCCGTTGTGTTTGTGCTCTT	2092
Qy	2374	GGCACCTCTGTCCCAG	2389
Db	2093	GGAACCTCGGTGCCAG	2108

RESULT 13

BX374548

LOCUS BX374548 941 bp mRNA linear EST 08-MAY-2003

DEFINITION BX374548 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens cDNA clone CS0DB006YD18 5-PRIME, mRNA sequence.

ACCESSION BX374548

VERSION BX374548.1 GI:30438490

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 941)

Qy 1045 AAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATC 1104
 |||
 Db 360 AAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATC 419

Qy 1105 CTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACC 1164
 |||
 Db 420 CTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACC 479

Qy 1165 GATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTG 1224
 |||
 Db 480 GATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTG 539

Qy 1225 GAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACC 1284
 |||
 Db 540 GAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACC 599

Qy 1285 ATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTC 1344
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 Db 600 ATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTC 659

Qy 1345 ACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATA 1404
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 Db 660 ACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATA 719

Qy 1405 ATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGC 1464
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 Db 720 ATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGNTAGGTTGAGCAATGTCCGC 779

Qy 1465 ATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTG 1524
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 Db 780 ATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTNNCAGCATATTCAAACAGTCTTCCCTTG 839

Qy 1525 CCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCAT 1584
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 Db 840 CCTCGGGCTGTCCTAGCCTNCCCTTGNGTGGNCACAGTTACCATCTTGGATGATGACCAT 899

Qy 1585 GCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG 1625
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 Db 900 GCNAGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG 940

RESULT 14

AY408695

LOCUS AY408695 2515 bp DNA linear GSS 12-DEC-2003

DEFINITION Mus musculus HCM3309 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY408695

VERSION AY408695.1 GI:39764666

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2515)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

TITLE	Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 2515)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

FEATURES	Location/Qualifiers
source	1..2515 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090"
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ORIGIN

Query Match 31.6%; Score 874.8; DB 29; Length 2515;
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Matches 1348; Conservative 0; Mismatches 708; Indels 52; Gaps 6;

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Qy	751	GCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACAC	810
Db	486	GCGGACAAGCGACTGCTCTTCTACAAGTACGTGTACAAGCGCTACCGCACCGACCCTCGC	545
Qy	811	CGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATGGGAAA	870
Db	546	AGTGAATCATCATCGGGGCAGAGGGAGACCACCCAAGAGCATCGAGCTGGACGGCACA	605
Qy	871	ATGATGAATTCCCATTTTCTAGATG-----GGAACCTGGTGCCCCTGGAAGGG	918
Db	606	TTCGTGGGCACTGAGGTCCCTGGCGAGCTGGGCGCATTGGGCACAGGTCCTGCTGAGGCG	665
Qy	919	AAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAA	978
Db	666	CGTGAAGTAGATGCCAGCCGGCGTGAGGTATCCAGATCCTTAAGGACTTGAAGCAGAAG	725
Qy	979	CACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCAC	1038
Db	726	CACCCGGATAAGGACCTGGAGCAGCTGATGGGCATCGCCAAGTACTATGCACTGCTGCAC	785
Qy	1039	CAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGC	1098
Db	786	CAGCAGAAGAGCCGCGCCTTCTACCGCATCCAGGCCACGCGGCTGATGACAGGTGCGGGC	845
Qy	1099	AATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCCTCCAGCATGAGCGAGGTG	1158

Db	846	AATGTGCTGCGCAGACATGCTGCGGATGCTGCCCCGAGGCCGGGAGCCACCGATGGTGCC	905
Qy	1159	CACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG	1218
Db	906	CCCATGATGAGGATGATGGTGCCAGTCGCA---TCTTCTTTGAGCCCAGCCTCTATCAC	962
Qy	1219	TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATGTCA	1278
Db	963	TGCCTGGAGAACTGCGGGTCAGTGCTGCTGTCCGTGGCTTGCCAGGGTGGTGAGGGCAAC	1022
Qy	1279	AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT	1338
Db	1023	AGCACCTTCTACGTGGACTACCGTACTGAGGACGGTTCTGCAAAGGCAGGCTCCGATTAT	1082
Qy	1339	GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG	1398
Db	1083	GAGTACAGCGAGGGCACACTGGTGTTCAGCCCGGGGAGACGCAGAAGGACCTGCGCATC	1142
Qy	1399	GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT	1458
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Qy	1459	GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT	1518
Db	1203	CTGCGTGTGGGCGATGCTCAGGGCATGTTTCGAG-----CCCGACGGCGGT	1247
Qy	1519	CCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGAT	1578
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Qy	1579	GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCACTGAGAGTATTGGT	1638
Db	1308	GACCACGCGGGCATCTTCTCCTTCCAGGACCGCCTGCTGCATGTGAGCGAGTGCATGGGC	1367
Qy	1639	GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGTACAGTCATCGTCCCCTTT	1698
Db	1368	ACTGTGGATGTGCGCGTGGTTCGAGCTCGGGCGCCCGTGGCACTGTACGCCTCCCCTAC	1427
Qy	1699	AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAG	1758
Db	1428	CGCACAGTGGACGGCACGGCCCGTGGCGGTGGTGTACATTACGAGGATGCTTGTGGAGAG	1487
Qy	1759	TTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAG	1818
Db	1488	CTGGAGTTCGGCGATGATGAGAC-CAGAAAACCTCTTCAGGTCAAGATAGTGGATGATGAA	1546
Qy	1819	GAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGT	1878
Db	1547	GAGTATGAGAAGAAGGACAACCTTCTTCATTGAGCTGGGCCAGCCCCAGTGGCTTAAGCGA	1606
Qy	1879	GGAATATCAGATGTGAC-----AGACAGGAAGCTGACTATGGAAGAA	1920
Db	1607	GGCATCTCAGNNNNNNNNNNNNNNNNNNNGGAATGGAGACAAGAAGATAACTGCAGAGCAG	1666
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980

Db 1667 GAGGAGGCCCCAGAGGATAGCAGAGATGGGCAAGCCAGTTCTTGGGGAGAACAATCGCCTC 1726
 Qy 1981 GAAGTCATCATTGAAGAGTCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG 2040
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 Qy 2158 TCCTGCTTTGACTACGTGATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGT 2217
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 Qy 2398 GCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACG 2457
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 Qy 2638 CACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTT 2697
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 Db 2387 CAGATTGGCGGCGAGCTGGGCGGCCCGCGGGGACCCAAGCTGGCCACCACCGCTCTCTTC 2446
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RESULT 15

BI913344

LOCUS BI913344 887 bp mRNA linear EST 16-OCT-2001

DEFINITION 603178823F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243308 5', mRNA sequence.

ACCESSION BI913344

VERSION BI913344.1 GI:16177710

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 887)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11613 row: m column: 05

High quality sequence stop: 782.

FEATURES

source

Location/Qualifiers

1. .887

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5243308"

/lab_host="DH10B"

/clone_lib="NIH_MGC_121"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: EcoRV (destroyed); RNA source anonymous pool of 3

fetal brains, female age 20 weeks, female age 24 weeks,

and male age 26 weeks. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

0.7-3.5 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 017. Note:

this is a NIH_MGC Library."

ORIGIN

Query Match 29.4%; Score 813.8; DB 12; Length 887;

Best Local Similarity 97.2%; Pred. No. 6.1e-189;

Matches 860; Conservative 0; Mismatches 22; Indels 3; Gaps 3;

Qy 916 GGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 975

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Db 1 GGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 60

Qy	976	AAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCC	1035
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Db	301	CAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATG	360
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Db	361	TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC	420
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Db	481	GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC	540
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Db	601	CTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT	660
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Db	661	GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTA-T	719
Qy	1636	GGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGTACAGTCATCGTCCCC	1695
Db	720	GGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGTACAGTCATCGTCCCC	779
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Db	780	TTTCAGGACAGGAGAAGGGACAGCCAAGGCTGCACGCTAAGGACTTGAAGACCCATATGC	839
Qy	1755	GGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGT	1799
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Job time : 6359.47 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 04:06:20 ; Search time 10407.3 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

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	2	2766	100.0	3812	6	AX496815		AX496815	Sequence
	3	2764.4	99.9	2966	6	AX480881		AX480881	Sequence
	4	2764.4	99.9	5250	9	AF510501		AF510501	Homo sapi
	5	2761.2	99.8	2782	6	AX476818		AX476818	Sequence
	6	2737.4	99.0	2837	9	HSA304853		AJ304853	Homo sapi
	7	2736.4	98.9	5268	9	AF510502		AF510502	Homo sapi
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	9	2657.6	96.1	2840	9	HSA304852		AJ304852	Homo sapi
	10	2546.4	92.1	5146	9	AF510503		AF510503	Homo sapi
	11	2398	86.7	4640	10	BC052435		BC052435	Mus muscu
	12	2352.4	85.0	4854	10	RNU53420		U53420	Rattus norv
	13	2312.8	83.6	3838	9	HSA508602		AJ508602	Homo sapi
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	22	1544	55.8	1784	10	AF321404		AF321404	Mus muscu
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	24	1326.4	48.0	2814	9	AF108389		AF108389	Homo sapi
	25	1326.4	48.0	2965	9	AF107593		AF107593	Macaca mu
	26	1326	47.9	6023	9	HSM808447		BX648299	Homo sapi
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38	1232	44.5	2874	10	AF109164	AF109164 Rattus no
39	1230.4	44.5	3303	10	RNU04933	U04933 Rattus norv
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41	1227.8	44.4	4087	6	AX360315	AX360315 Sequence
42	1227	44.4	3126	10	RNSCEA2	X68813 R.norvegicu
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ALIGNMENTS

RESULT 1

AX496811

LOCUS AX496811 2766 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 1 from Patent WO02059316.

ACCESSION AX496811

VERSION AX496811.1 GI:23342335

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hilbun,E. and Friddle,C.J.

TITLE Human ion exchanger proteins and polynucleotides encoding the same

JOURNAL Patent: WO 02059316-A 1 01-AUG-2002;

LEXICON GENETICS INC (US)

FEATURES

Location/Qualifiers

source

1. .2766

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ORIGIN

Query Match 100.0%; Score 2766; DB 6; Length 2766;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	901		CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901		CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
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Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
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Db	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920

Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
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Db	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
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Db	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Db	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Qy	2341	GATTTCAGTCACAGCTGTTGTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2341	GATTTCAGTCACAGCTGTTGTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Qy	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCACGTGTGCGCCGGCACACTGGCCTTCTCCGTCAAC	2580
Db	2521	TGGGCTCTGCAGGGACAGGAGTTCACGTGTGCGCCGGCACACTGGCCTTCTCCGTCAAC	2580
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGCGGCCGCAC	2640
Db	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGCGGCCGCAC	2640
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Qy	2701	AGCCTGTGGCTCCTCTACATACTCTTGGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Db	2701	AGCCTGTGGCTCCTCTACATACTCTTGGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760

Qy 2761 TTCTAA 2766
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Db 2761 TTCTAA 2766

RESULT 2

AX496815

LOCUS AX496815 3812 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 5 from Patent WO02059316.

ACCESSION AX496815

VERSION AX496815.1 GI:23342337

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hilbun, E. and Friddle, C.J.

TITLE Human ion exchanger proteins and polynucleotides encoding the same

JOURNAL Patent: WO 02059316-A 5 01-AUG-2002;

LEXICON GENETICS INC (US)

FEATURES Location/Qualifiers

source

1. 3812

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2766; DB 6; Length 3812;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db 618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db 678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy 121 ACAGGGCAGAACAAATGAGTCCTGTT CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db 738 ACAGGGCAGAACAAATGAGTCCTGTT CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 797

Qy 181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db 798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy 241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300
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Db 858 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 917

Qy 301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
|||||
Db 918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy 361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420

Db	978		ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	1037
Qy	421		CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	1038		CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	1097
Qy	481		ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1098		ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1157
Qy	541		ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1158		ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1217
Qy	601		CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1218		CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1277
Qy	661		CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1278		CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1337
Qy	721		TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1338		TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1397
Qy	781		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1398		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1457
Qy	841		CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1458		CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1517
Qy	901		CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1518		CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1577
Qy	961		AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1578		AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1637
Qy	1021		TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1638		TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1697
Qy	1081		ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1698		ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1757
Qy	1141		TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1758		TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1817
Qy	1201		GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260

Db	1818	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1877
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1878	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1937
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1938	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1997
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1998	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2057
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2058	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2117
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	2118	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	2177
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	2178	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	2237
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	2238	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	2297
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2298	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2357
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	2358	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	2417
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	2418	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	2477
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	2478	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	2537
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	2538	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	2597
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAGACTACGGTGGACAACTGATCAAGAAG	2040
Db	2598	GAAGTCATCATTGAAGAGTCCTATGAGTTCAGACTACGGTGGACAACTGATCAAGAAG	2657
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Db	2658	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2717

Qy 2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
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 Db 2718 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2777

Qy 2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
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 Db 2778 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2837

Qy 2221 CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
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 Db 2838 CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2897

Qy 2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA 2340
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 Db 2898 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA 2957

Qy 2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTGGCACCTCTGTCCCAGATACGTTTGCC 2400
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 Db 2958 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTGGCACCTCTGTCCCAGATACGTTTGCC 3017

Qy 2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
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 Db 3018 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 3077

Qy 2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
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 Db 3078 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 3137

Qy 2521 TGGGCTCTGCAGGGACAGGAGTTCACGTGTCGGCCGGCACACTGGCCTTCTCCGTACCC 2580
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 Db 3138 TGGGCTCTGCAGGGACAGGAGTTCACGTGTCGGCCGGCACACTGGCCTTCTCCGTACCC 3197

Qy 2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
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 Db 3198 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 3257

Qy 2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
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 Db 3258 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 3317

Qy 2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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 Db 3318 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 3377

Qy 2761 TTCTAA 2766
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 Db 3378 TTCTAA 3383

RESULT 3

AX480881

LOCUS AX480881 2966 bp DNA linear PAT 12-AUG-2002
 DEFINITION Sequence 41 from Patent WO0246415.
 ACCESSION AX480881
 VERSION AX480881.1 GI:22217538
 KEYWORDS .

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Lee,E.A., Baughn,M.R., Yue,H., Ding,L., Raumann,B.E., Hafalia,A.J.,
 Khan,F.A., Nguyen,D.B., Elliott,V.S., Ramkumar,J., Walia,N.K.,
 Ison,C.H., Lu,Y., Gandhi,A.R., Warren,B.A., Duggan,B.M.,
 Tribouley,C.M., Burford,N., Lu,D.A., Lal,P.G., Yao,M.G., Xu,Y.,
 Bruns,C.M., Thangavelu,K., Swarnakar,A., Tang,Y.T., Azimzai,Y.,
 Thornton,M., Arvizu,C. and Policky,J.L.
 TITLE Transporters and ion channels
 JOURNAL Patent: WO 0246415-A 41 13-JUN-2002;
 Incyte Genomics, Inc. (US)
 FEATURES Location/Qualifiers
 source 1. .2966
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="Incyte ID No: 5923789CB1"

ORIGIN

Query Match 99.9%; Score 2764.4; DB 6; Length 2966;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	261	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	320
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	321	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	380
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	381	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	440
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	441	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	500
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	501	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	560
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	561	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	620
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	621	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	680

Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	681	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	740
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	741	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	800
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	801	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	860
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	861	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	920
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	921	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	980
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	981	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1040
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Db	1041	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	1100
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1101	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1160
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1161	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1220
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1221	TACTATGCTCTTTCCACCAACAGAAGAGCCCTTCTACCGTATCCAAGCCACTCGT	1280
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1281	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1340
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1341	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1400
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1401	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1460
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1461	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1520

Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1521	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1580
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1581	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1640
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1641	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1700
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1701	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1760
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1761	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1820
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1821	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1880
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1881	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1940
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1941	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	2000
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	2001	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	2060
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	2061	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	2120
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	2121	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	2180
Qy	1981	GAAGTCATCATTGAAGAGTCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	2181	GAAGTCATCATTGAAGAGTCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2240
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Db	2241	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2300
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2301	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2360
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220

Db	2361		2420
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2421	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2480
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2340
Db	2481	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2540
Qy	2341	GATTCAAGTACAGCTGTTGTTTTCGTGGCATTGGCACCTCTGTCCCAGATACGTTTGCC	2400
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Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2601	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2660
Qy	2461	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2661	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2720
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2721	TGGGCTCTGCAGGGACAGGAGTTCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2780
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGCCGCAC	2640
Db	2781	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGCCGCAC	2840
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2841	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2900
Qy	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Db	2901	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2960
Qy	2761	TTCTAA	2766
Db	2961	TTCTAA	2966

RESULT 4

AF510501

LOCUS AF510501 5250 bp mRNA linear PRI 30-OCT-2002

DEFINITION Homo sapiens Na⁺/Ca²⁺ exchanger isoform 3 splice variant 2 (SLC8A3) mRNA, complete cds; alternatively spliced.

ACCESSION AF510501

VERSION AF510501.1 GI:24421220

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5250)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
 TITLE The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+) exchanger 3 isoforms
 JOURNAL Gene 298 (1), 1-7 (2002)
 MEDLINE 22294016
 PUBMED 12406570
 REFERENCE 2 (bases 1 to 5250)
 AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAY-2002) Department of Biology, Univ. of Padova, via G. Colombo, Padova, PD 35131, Italy
 FEATURES
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 CDS 755. .3520
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 Query Match 99.9%; Score 2764.4; DB 9; Length 5250;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	815	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	874
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG	180
Db	875	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG	934
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	935	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	994
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	995	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	1054
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	1055	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	1114
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	1115	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	1174
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	1175	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	1234
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1235	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1294
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1355	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1414
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
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Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1475	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1534
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1535	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1594
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900

Db	1595	 CACCCTAAGGGCATTGAGATGGATGGGAAATGATGAATTCCCATTCTCTAGATGGGAAC	1654
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1655	 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1714
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1715	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1774
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1775	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1834
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1835	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1894
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1895	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1954
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1955	 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	2014
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	2015	 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	2074
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	2075	 AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	2134
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	2135	 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2194
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCCTCA	1500
Db	2195	 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCCTCA	2254
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	2255	 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA	2314
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	2315	 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	2374
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	2375	 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	2434
Qy	1681	ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740

Db	2435	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2494
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
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Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	2675	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	2734
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Db	2735	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2794
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
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Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2855	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2914
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2915	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2974
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2975	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	3034
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Db	3035	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	3094
Qy	2341	GATTTCAGTCACAGCTGTTGTTTTCTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
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Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
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Qy	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	3215	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	3274
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGGCACACTGGCCTTCTCCGTCAAC	2580
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Qy 2701 AGCCTGTGGCTCCTCTACATACTCTTGGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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Qy 2761 TTCTAA 2766
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RESULT 5

AX476818

LOCUS AX476818 2782 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 1 from Patent WO0233086.

ACCESSION AX476818

VERSION AX476818.1 GI:22216098

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Merkulov,G.V., Ketchum,K.A., Shao,W., Yan,C., di Francesco,V. and
 Beasley,E.M.

TITLE Isolated human transporter proteins, nucleic acid molecules
 encoding human transporter proteins, and uses thereof

JOURNAL Patent: WO 0233086-A 1 25-APR-2002;
 PE Corporation (NY) (US)

FEATURES Location/Qualifiers
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ORIGIN

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Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db 310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369

Qy 361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db 490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 549

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Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
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Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
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Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
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Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
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Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
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Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
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Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
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Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
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Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1690	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1749
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1750	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1809
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1810	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1869

Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1870	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1929
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA	1980
Db	1930	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTG	1989
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	1990	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2049
Qy	2041	ACAAACCTGGCCTTGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2050	ACAAACCTGGCCTTGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC	2109
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2110	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2169
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2170	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2229
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2230	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2289
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2340
Db	2290	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2349
Qy	2341	GATTTCAGTCACAGCTGTTGTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2350	GATTTCAGTCACAGCTGTTGTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC	2409
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2410	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2469
Qy	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2470	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2529
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACACTGGCCTTCTCCGTACAC	2580
Db	2530	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACACTGGCCTTCTCCGTACAC	2589
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2590	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2649
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2650	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2709
Qy	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2710 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2769
Qy      2761 TTCTAA 2766
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Db      2770 TTCTAA 2775

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RESULT 6

HSA304853

LOCUS HSA304853 2837 bp mRNA linear PRI 06-JUN-2001

DEFINITION Homo sapiens mRNA for sodium/calcium exchanger, SCL8A3, alternative splice form B (SCL8A3 gene).

ACCESSION AJ304853

VERSION AJ304853.1 GI:14330384

KEYWORDS alternative splicing; form B; SCL8A3 gene; SCL8A3 protein; Sodium/calcium exchanger.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Gabellini, N.

TITLE Characterization of the human SCL8A3 gene for solute carrier family 8, member 3 (sodium/calcium exchanger)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2837)

AUTHORS Bortoluzzi, S.

TITLE Direct Submission

JOURNAL Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and Department of Biological Chemistry, University of Padova, via G. Colombo 3, 35131 PADOVA, ITALY

FEATURES

source

Location/Qualifiers

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1. .2837
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CDS

63. .2837
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/function="sodium/calcium exchanger"
/note="alternative splice form B (exons 2, 4, 5, 9, 10, 11, 12)"
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/db_xref="SPTREMBL:Q96QG1"
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ORIGIN

Query Match 99.0%; Score 2737.4; DB 9; Length 2837;
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 Matches 2760; Conservative 0; Mismatches 6; Indels 9; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
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Qy	61	TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	123	TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	182
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	183	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	242
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	243	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	302
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	303	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	362
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	363	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	422
Qy	361	ACCAGCACAACCACTATTGGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	423	ACCAGCACAACCACTATTGGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	482
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	483	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	542
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	543	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	602
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	603	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	662

Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	663	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	722
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	723	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	782
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	783	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	842
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	843	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	902
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	903	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	962
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	963	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1022
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1023	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1082
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1083	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1142
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1143	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1202
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1203	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1262
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1263	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1322
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1323	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1382
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1383	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1442
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1443	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1502

Qy	1441	TTTGTAAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1503	TTTGTAAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1562
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1563	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1622
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1623	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1682
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1683	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1742
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1743	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1802
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1803	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGTGAAAACCATAAGGGTT	1862
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1863	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1922
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGT-----GACAGACAGGAAGCTGACT	1911
Db	1923	CCGAAATGGATGGAACGTGGAATATCAGCGCTCCTGTTATCTCCAGACAGGAAGCTGACT	1982
Qy	1912	ATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACAC	1971
Db	1983	ATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACAC	2042
Qy	1972	CCCAAAGTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTG	2031
Db	2043	CCCAAAGTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTG	2102
Qy	2032	ATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATG	2091
Db	2103	ATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATG	2162
Qy	2092	GAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGG	2151
Db	2163	GAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGG	2222
Qy	2152	CTGCCCTCCTGCTTTGACTACGTCATGCACCTTCTGACTGTCTTCTGGAAGGTGCTGTTT	2211
Db	2223	CTGCCCTCCTGCTTTGACTACGTCATGCACCTTCTGACTGTCTTCTGGAAGGTGCTGTTT	2282
Qy	2212	GCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTC	2271
Db	2283	GCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTC	2342
Qy	2272	ATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATT	2331

Db	2343		ATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATT	2402
Qy	2332		GGTCTCAAAGATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTTCGGCACCTCTGTCCCAGAT	2391
Db	2403		GGTCTCAAAGATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTTCGGCACCTCTGTCCCAGAT	2462
Qy	2392		ACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAAC	2451
Db	2463		ACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAAC	2522
Qy	2452		GTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCC	2511
Db	2523		GTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCC	2582
Qy	2512		GCCATCTACTGGGCTCTGCAGGGACAGGAGTTCACGTGTGGCCGGCACACTGGCCTTC	2571
Db	2583		GCCATCTACTGGGCTCTGCAGGGACAGGAGTTCACGTGTGGCCGGCACACTGGCCTTC	2642
Qy	2572		TCCGTCAACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGG	2631
Db	2643		TCCGTCAACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGG	2702
Qy	2632		CGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGG	2691
Db	2703		CGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGG	2762
Qy	2692		CTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTAC	2751
Db	2763		CTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTAC	2822
Qy	2752		ATCAAGGGGTTCTAA	2766
Db	2823		ATCAAGGGGTTCTAA	2837

RESULT 7
AF510502

LOCUS	AF510502	5268 bp	mRNA	linear	PRI 30-OCT-2002
DEFINITION	Homo sapiens Na ⁺ /Ca ²⁺ exchanger isoform 3 splice variant 3 (SLC8A3) mRNA, complete cds; alternatively spliced.				
ACCESSION	AF510502				
VERSION	AF510502.1 GI:24421222				
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 5268)				
AUTHORS	Gabellini, N., Bortoluzzi, S., Danieli, G.A. and Carafoli, E.				
TITLE	The human SLC8A3 gene and the tissue-specific Na ⁽⁺⁾ /Ca ⁽²⁺⁾ exchanger 3 isoforms				
JOURNAL	Gene 298 (1), 1-7 (2002)				
MEDLINE	22294016				
PUBMED	12406570				
REFERENCE	2 (bases 1 to 5268)				
AUTHORS	Gabellini, N., Bortoluzzi, S., Danieli, G.A. and Carafoli, E.				

Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	875	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	934
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	935	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	994
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	995	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	1054
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	1055	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	1114
Qy	361	ACCAGCACAAACCACTATTCCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	1115	ACCAGCACAAACCACTATTCCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	1174
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	1175	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	1234
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1235	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1294
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1295	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1354
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1355	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1414
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	1415	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	1474
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1475	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1534
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1535	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1594
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1595	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1654
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1655	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1714
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020

Db	1715	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1774
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1775	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1834
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Db	1835	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1894
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1895	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1954
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1955	 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	2014
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	2015	 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	2074
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	2075	 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	2134
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	2135	 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2194
Qy	1441	TTTGTAAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2195	 TTTGTAAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2254
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	2255	 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	2314
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	2315	 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	2374
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	2375	 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	2434
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2435	 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2494
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Db	2675	AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG	2734
Qy	1963	GGTGAACACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG	2022
Db	2735	GGTGAACACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG	2794
Qy	2023	GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGAC	2082
Db	2795	GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGAC	2854
Qy	2083	CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG	2142
Db	2855	CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG	2914
Qy	2143	GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG	2202
Db	2915	GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG	2974
Qy	2203	GTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC	2262
Db	2975	GTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC	3034
Qy	2263	TCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGC	2322
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Qy	2323	TGCACCATTGGTCTCAAAGATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCT	2382
Db	3095	TGCACCATTGGTCTCAAAGATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCT	3154
Qy	2383	GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC	2442
Db	3155	GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC	3214
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Qy	2503	TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCACGTGTGCGCCGGCACA	2562
Db	3275	TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCACGTGTGCGCCGGCACA	3334
Qy	2563	CTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG	2622
Db	3335	CTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG	3394
Qy	2623	TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC	2682
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Qy 2683 ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC 2742
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RESULT 8

AX299471

LOCUS AX299471 2781 bp DNA linear PAT 26-NOV-2001

DEFINITION Sequence 1 from Patent WO0183744:

ACCESSION AX299471

VERSION AX299471.1 GI:17129228

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Wilm, C.

TITLE Natrium-calcium exchanger protein

JOURNAL Patent: WO 0183744-A 1 08-NOV-2001;

MERCK PATENT GmbH (DE)

FEATURES

Location/Qualifiers

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CDS

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ORIGIN

Query Match

98.8%; Score 2733.4; DB 6; Length 2781;

Best Local Similarity 99.3%; Pred. No. 0;
Matches 2762; Conservative 0; Mismatches 1; Indels 18; Gaps 1;

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Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
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Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCAATGGAGAA	360
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Qy	361	ACCAGCACAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
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Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
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Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
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Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
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Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
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Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
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Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
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Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
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Qy	2143	GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG	2202
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Qy	2323	TGCACCATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTCGTGGCATTGTCACCTCT	2382
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Qy	2383	GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC	2442
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Qy	2443	ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGG	2502
Db	2461	ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGG	2520

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RESULT 9

HSA304852

LOCUS HSA304852 2840 bp mRNA linear PRI 06-JUN-2001

DEFINITION Homo sapiens mRNA for sodium/calcium exchanger SCL8A3, alternative splice form A (SCL8A3 gene).

ACCESSION AJ304852

VERSION AJ304852.1 GI:14330382

KEYWORDS alternative splicing; form A; SCL8A3 gene; SCL8A3 protein; Sodium/calcium exchanger.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS Gabellini,N.

TITLE Characterization of the human SCL8A3 gene for solute carrier family 8, member 3 (sodium/calcium exchanger)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2840)

AUTHORS Bortoluzzi,S.

TITLE Direct Submission

JOURNAL Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and Department of Biological Chemistry, University of Padova, via G. Colombo 3, 35131 PADOVA, ITALY

FEATURES

Location/Qualifiers

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63. .2840

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Db	1023	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1082
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Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
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Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1383	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1442
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1443	CAGAAGGAGTTCTCCGTGGGCATAAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1502
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1503	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1562
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1563	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1622
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1623	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1682
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1683	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1742
Qy	1681	ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1743	ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1802
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1803	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACAATTACATC	1862
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1863	AAGGTAATTGATGATGAGGCATATGAGAAAAACAAGAATTACTTCATTGAGATGATGGGC	1922
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTG-----ACAGACAGGAAGCTG	1908
Db	1923	CCCCGCATGGTGGATATGAGTTTTTCAGAAAGCGCTCCTGTTATCTCCAGACAGGAAGCTG	1982
Qy	1909	ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA	1968
Db	1983	ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA	2042
Qy	1969	CACCCCAAAC TAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAA	2028
Db	2043	CACCCCAAAC TAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAA	2102
Qy	2029	CTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTC	2088
Db	2103	CTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTC	2162

Qy	2089	ATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAG	2148
Db	2163	ATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAG	2222
Qy	2149	AGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTG	2208
Db	2223	AGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTG	2282
Qy	2209	TTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATC	2268
Db	2283	TTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATC	2342
Qy	2269	CTCATCATTTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACC	2328
Db	2343	CTCATCATTTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACC	2402
Qy	2329	ATTGGTCTCAAAGATTCACTCACAGCTGTTGTTTTCTGTTGGCATTGGCACCTCTGTCCCA	2388
Db	2403	ATTGGTCTCAAAGATTCACTCACAGCTGTTGTTTTCTGTTGGCATTGGCACCTCTGTCCCA	2462
Qy	2389	GATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGC	2448
Db	2463	GATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGC	2522
Qy	2449	AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG	2508
Db	2523	AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG	2582
Qy	2509	GCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCC	2568
Db	2583	GCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCC	2642
Qy	2569	TTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGA	2628
Db	2643	TTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGA	2702
Qy	2629	AGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACA	2688
Db	2703	AGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACA	2762
Qy	2689	TGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGC	2748
Db	2763	TGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGC	2822
Qy	2749	TACATCAAGGGGTTCTAA	2766
Db	2823	TACATCAAGGGGTTCTAA	2840

RESULT 10

AF510503

LOCUS AF510503 5146 bp mRNA linear PRI 30-OCT-2002

DEFINITION Homo sapiens Na⁺/Ca²⁺ exchanger isoform 3 splice variant 4 (SLC8A3) mRNA, complete cds; alternatively spliced.

ACCESSION AF510503

VERSION AF510503.1 GI:24421224

KEYWORDS .

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5146)
 AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
 TITLE The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+) exchanger 3 isoforms
 JOURNAL Gene 298 (1), 1-7 (2002)
 MEDLINE 22294016
 PUBMED 12406570

REFERENCE 2 (bases 1 to 5146)
 AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAY-2002) Department of Biology, Univ. of Padova, via G. Colombo, Padova, PD 35131, Italy

FEATURES
 Location/Qualifiers
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 /mol_type="mRNA"
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 /map="14q24.2"
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 5'UTR 1. .754
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 CDS 755. .2617
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 polyA_signal 5117. .5122
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ORIGIN

Query Match 92.1%; Score 2546.4; DB 9; Length 5146;
 Best Local Similarity 96.2%; Pred. No. 0;
 Matches 2661; Conservative 0; Mismatches 1; Indels 104; Gaps 1;

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Db	755	 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC	814
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	815	 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	874
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	875	 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	934
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	935	 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	994
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	995	 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	1054
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	1055	 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	1114
Qy	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	1115	 ACCAGCACAAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	1174
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	1175	 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	1234
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1235	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1294
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1295	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1354
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1355	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1414
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1415	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1474
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1475	 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1534
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1535	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1594
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900

Db	1595	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1654
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1655	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1714
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1715	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1774
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1775	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1834
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1835	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1894
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1895	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1954
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1955	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	2014
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	2015	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	2074
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	2075	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	2134
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	2135	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2194
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2195	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2254
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	2255	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	2314
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	2315	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	2374
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	2375	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	2434
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2435	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2494

Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	2495	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGT-----	2538
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	2539	-----	2538
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	2539	-----ATGTGACAGACAGGAAGCTGACTATGGAAGAA	2570
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	2571	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	2630
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	2631	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2690
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2691	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC	2750
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2751	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2810
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2811	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2870
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2871	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2930
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA	2340
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Db	3051	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	3110
Qy	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
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Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCACGTGTGGCCGGCACACTGGCCTTCTCCGTCAAC	2580
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 Db 3231 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 3290

Qy 2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
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 Db 3291 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 3350

Qy 2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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 Db 3351 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 3410

Qy 2761 TTCTAA 2766
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 Db 3411 TTCTAA 3416

RESULT 11

BC052435

LOCUS BC052435 4640 bp mRNA linear ROD 07-OCT-2003

DEFINITION Mus musculus solute carrier family 8 (sodium/calcium exchanger), member 3, mRNA (cDNA clone MGC:63358 IMAGE:6837128), complete cds.

ACCESSION BC052435

VERSION BC052435.1 GI:30851384

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4640)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 4640)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (15-MAY-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.

Web site: <http://genome.uiowa.edu>

Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu

Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A., Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K., Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J., Casavant, T., Soares, M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: Plate: Row: Column: 0.

FEATURES

source

Location/Qualifiers

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gene

1. .4640

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CDS

373. .3138

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ORIGIN

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Query Match          86.7%;  Score 2398;  DB 10;  Length 4640;
Best Local Similarity 91.7%;  Pred. No. 0;
Matches 2536;  Conservative 0;  Mismatches 230;  Indels 0;  Gaps 0;

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 Db 3133 TTCTGA 3138

RESULT 12

RNU53420

LOCUS RNU53420 4854 bp mRNA linear ROD 04-OCT-1996

DEFINITION Rattus norvegicus sodium-calcium exchanger form 3 (NCX3) mRNA, complete cds.

ACCESSION U53420

VERSION U53420.1 GI:1552525

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 4854)
 AUTHORS Nicoll,D.A., Quednau,B.D., Qui,Z., Xia,Y.R., Lysis,A.J. and
 Philipson,K.D.
 TITLE Cloning of a third mammalian Na⁺-Ca²⁺ exchanger, NCX3
 JOURNAL J. Biol. Chem. 271 (40), 24914-24921 (1996)
 MEDLINE 96394663
 PUBMED 8798769
 REFERENCE 2 (bases 1 to 4854)
 AUTHORS Nicoll,D.A. and Philipson,K.D.
 TITLE Direct Submission
 JOURNAL Submitted (02-APR-1996) Physiology, University of California, Los
 Angeles, 3645 MRLB, 675 Circle Dr. S., Los Angeles, CA 90095-1760,
 USA

FEATURES Location/Qualifiers
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ORIGIN

Query Match

85.0%; Score 2352.4; DB 10; Length 4854;

Best Local Similarity 90.7%; Pred. No. 0;
Matches 2525; Conservative 0; Mismatches 241; Indels 18; Gaps 1;

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Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
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Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
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Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
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Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	2634	AAAATAGTAGATGAGGAGGAGTACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	2693
Qy	1861	CCGAAATGGATGGAACGTGGAATAT-----CAGATGTGACAGACAGG	1902
Db	2694	CCGAAATGGATGGAACGTGGAATATCAGCGCTCCTGTTATCTCCAGAGGTGACAGACAGG	2753
Qy	1903	AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG	1962
Db	2754	AAGCTGACTATGGAGGAAGAGGAGGCCAAGAGAATAGCAGAGATGGGAAAGCCAGTATTG	2813
Qy	1963	GGTGAACACCCCAAAC TAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG	2022
Db	2814	GGTGAACACCCCTAAACTAGAGGTCATCATTGAAGAGTCCTATGAGTTCAAGAGTACAGTG	2873
Qy	2023	GACAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGAC	2082
Db	2874	GATAAACTGATCAAGAAGACAAACCTGGCATTGGTTGTGGGGACCCATTCTGGAGGGAC	2933
Qy	2083	CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG	2142
Db	2934	CAATTCATGGAAGCCATCACTGTTAGTGCAGCAGGAGATGAGGAGGAAGATGAATCTGGA	2993
Qy	2143	GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG	2202
Db	2994	GAGGAGAGGCTGCCATCATGCTTTGACTATGTCATGCACTTCCTGACGGTCTTTTGGGAAG	3053
Qy	2203	GTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC	2262
Db	3054	GTGCTCTTTGCCTGTGTGCCCCCACAGAGTACTGCCATGGCTGGGCCTGCTTCGTGGTC	3113
Qy	2263	TCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGC	2322
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Qy	2323	TGCACCATTGGTCTCAAAGATTCACTCACAGCTGTTGTTTTCGTGGCATTTCGGCACCTCT	2382
Db	3174	TGCACCATCGGGCTCAAGGATTTCGGTCACAGCTGTTGTTTTGTGGCATTTCGGCACCTCT	3233
Qy	2383	GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC	2442
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ORIGIN

Query Match 83.6%; Score 2312.8; DB 9; Length 3838;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2314; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy	511	GTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCA	570
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Qy	571	GACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGT	630
Db	121	GACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGT	180
Qy	631	ATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAG	690
Db	181	ATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAG	240
Qy	691	GTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGCTTCTGGCCTGGGTG	750
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Qy	751	GCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAGTACCGCACAGACAAACAC	810
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Qy	811	CGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATGGGAAA	870
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Qy	871	ATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAGTGGAT	930
Db	421	ATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAGTGGAT	480
Qy	931	GAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAGAGAAG	990
Db	481	GAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAGAGAAG	540
Qy	991	GACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAACAGAAGAGC	1050

Db	541	 GACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAACAGAAGAGC	600
Qy	1051	CGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCTGAAG	1110
Db	601	 CGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCTGAAG	660
Qy	1111	AAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAG	1170
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Qy	1351	GGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGAT	1410
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Qy	1411	GACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAG	1470
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Qy	1531	GCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGC	1590
Db	1081	 GCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGC	1140
Qy	1591	ATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTATGGAGGTC	1650
Db	1141	 ATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTATGGGGGTC	1200
Qy	1651	AAGGTTCTGCGGACATCAGGTGCCCAGGGGTACAGTCATCGTCCCCTTTAGGACAGTAGAA	1710
Db	1201	 AAGGTTCTGCGGACATCAGGTGCCCAGGGGTACAGTCATCGTCCCCTTTAGGACAGTAGAA	1260
Qy	1711	GGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTCAAG	1770
Db	1261	 GGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTCAAG	1320
Qy	1771	AATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACGAAAGG	1830
Db	1321	 AATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACGAAAGG	1380
Qy	1831	CAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATATCAGAT	1890

Db	1381	CAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATATCAGAT	1440
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Qy	1951	AAGCCAGTATTGGGTGAACACCCCAAAGTCAAGATCATCATTGAAGAGTCCTATGAGTTC	2010
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Qy	2011	AAGACTACGGTGGACAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCAT	2070
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Qy	2071	TCCTGGAGGGACCAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAG	2130
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Qy	2131	GATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACT	2190
Db	1681	GATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACT	1740
Qy	2191	GTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCC	2250
Db	1741	GTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCC	1800
Qy	2251	TGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCC	2310
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Qy	2311	TCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTCGTGGCA	2370
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Qy	2551	TCGGCCGGCACAACCTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATC	2610
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Qy	2611	AGCGTGCTCTTGTACCGAAGGCGGCCGACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGC	2670
Db	2161	AGCGTGCTCTTGTACCGAAGGCGGCCGACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGC	2220
Qy	2671	TGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCC	2730
Db	2221	TGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCC	2280

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RESULT 14

AF453257

LOCUS AF453257 3435 bp mRNA linear ROD 10-DEC-2001

DEFINITION Mus musculus sodium/calcium exchanger (Slc8a3) mRNA, complete cds.

ACCESSION AF453257

VERSION AF453257.1 GI:17432810

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3435)

AUTHORS Kraev,A.

TITLE Towards complete inventory of calcium transporters of the house
 mouse

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3435)

AUTHORS Kraev,A.

TITLE Direct Submission

JOURNAL Submitted (27-NOV-2001) Mt. Sinai Hospital, Samuel Lunenfeld
 Research Institute, 600 University Avenue, Toronto, Ontario M5G
 1X5, Canada

FEATURES Location/Qualifiers

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ORIGIN

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Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
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Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
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Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
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Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
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Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
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Qy 1861 CCGAAATGGATGGAACGTGGAATAT-----CAGATGTGACAGAC 1899
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ORIGIN

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Query Match          64.6%;  Score 1786.4;  DB 9;  Length 2534;
Best Local Similarity 99.9%;  Pred. No. 0;
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Qy	1621		GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 00:42:04 ; Search time 970.401 Seconds
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Title: US-10-054-680-1
Perfect score: 2766
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

ABQ78861

ID ABQ78861 standard; cDNA; 2766 BP.

XX

AC ABQ78861;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;

KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;

KW gene; ss; chromosome 14.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .2766

FT /*tag= a

FT /product= "Ion exchanger protein 1"

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

DR P-PSDB; ABB81913.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.

XX

PS Claim 1; Page 36-37; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence encodes a NHIEP of the invention

XX

SQ Sequence 2766 BP; 655 A; 678 C; 760 G; 673 T; 0 U; 0 Other;

Query Match 100.0%; Score 2766; DB 6; Length 2766;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

|||||

Db 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy 121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180

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Db	1681	 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1741	 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1801	 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920

Db	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Db	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Db	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Db	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Qy	2341	GATTCAGTCACAGCTGTTGTTTTCTGGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2341	GATTCAGTCACAGCTGTTGTTTTCTGGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC	2400
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Qy	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCACGTGTCGGCCGGCACACTGGCCTTCTCCGTACCC	2580
Db	2521	TGGGCTCTGCAGGGACAGGAGTTCACGTGTCGGCCGGCACACTGGCCTTCTCCGTACCC	2580
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Qy	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Db	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760

Qy 2761 TTCTAA 2766
 |||||
Db 2761 TTCTAA 2766

RESULT 2

ABQ78863

ID ABQ78863 standard; cDNA; 3812 BP.

XX

AC ABQ78863;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein cDNA #3.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW gene; ss; chromosome 14.

XX

OS Homo sapiens.

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.

XX

PS Disclosure; Page 41-42; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence encodes a NHIEP of the invention, with regions of flanking
CC sequence

XX

SQ Sequence 3812 BP; 860 A; 1059 C; 1041 G; 852 T; 0 U; 0 Other;

Query Match

100.0%; Score 2766; DB 6; Length 3812;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy     121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     738 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 797

Qy     181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy     241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     858 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 917

Qy     301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy     361 ACCAGCACAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     978 ACCAGCACAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC 1037

Qy     421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1038 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 1097

Qy     481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1098 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 1157

Qy     541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1158 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1217

Qy     601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1218 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1277

Qy     661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1278 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1337

Qy     721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1338 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1397

Qy     781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db	1398	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1457
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1458	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1517
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1518	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1577
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1578	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1637
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1638	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1697
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1698	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1757
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1758	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1817
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1818	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1877
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1878	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1937
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1938	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1997
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1998	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2057
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2058	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2117
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	2118	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	2177
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	2178	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	2237
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	2238	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	2297

Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2298	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2357
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	2358	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	2417
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	2418	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	2477
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	2478	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	2537
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	2538	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	2597
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	2598	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2657
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTTGGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2658	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTTGGAGGGACCAGTTCATGGAGGCCATC	2717
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2718	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2777
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2778	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2837
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2838	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2897
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Db	2898	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2957
Qy	2341	GATTTCAGTCACAGCTGTTGTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2958	GATTTCAGTCACAGCTGTTGTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC	3017
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	3018	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	3077
Qy	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	3078	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	3137

Qy 2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGGCACACTGGCCTTCTCCGTCACC 2580
 |||||
 Db 3138 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGGCACACTGGCCTTCTCCGTCACC 3197

Qy 2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
 |||||
 Db 3198 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 3257

Qy 2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
 |||||
 Db 3258 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 3317

Qy 2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
 |||||
 Db 3318 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 3377

Qy 2761 TTCTAA 2766
 |||||
 Db 3378 TTCTAA 3383

RESULT 3

ABQ78864

ID ABQ78864 standard; cDNA; 2766 BP.

XX

AC ABQ78864;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA A/G mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW gene; ss; mutant.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT mutation replace(1889,A)

FT /*tag= a

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are

PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.

XX

PS Disclosure; Page; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)

XX

SQ Sequence 2766 BP; 654 A; 678 C; 761 G; 673 T; 0 U; 0 Other;

Query Match 99.9%; Score 2764.4; DB 6; Length 2766;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540

Db	481	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Db	841	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380

Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Qy	1981	GAAGTCATCATTGAAGAGTCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Db	1981	GAAGTCATCATTGAAGAGTCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Db	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220

Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Db	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Qy	2341	GATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2341	GATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Qy	2461	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2461	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCACGTGTGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2521	TGGGCTCTGCAGGGACAGGAGTTCACGTGTGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Qy	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Db	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Qy	2761	TTCTAA	2766
Db	2761	TTCTAA	2766

RESULT 4

ABZ33735

ID ABZ33735 standard; cDNA; 2966 BP.

XX

AC ABZ33735;

XX

DT 30-JAN-2003 (first entry)

XX

DE Human TRICH encoding cDNA SEQ ID NO 41.

XX

KW Human; TRICH; transporter and ion channel; transport disorder;
 KW cystic fibrosis; diabetes mellitus; Parkinson's disease; cancer;
 KW neurological disorder; Alzheimer's disease; Huntington's disease;
 KW immunological disorder; AIDS; asthma; cell proliferative disorder;
 KW transgenic; gene therapy; neuroprotective; antidiabetic; cytostatic;

KW antiparkinsonian; hypotensive; nootropic; antianaemic; anticonvulsant;
KW cerebroprotective; cardiant; anti-HIV; human immunodeficiency virus;
KW antiasthmatic; antiatherosclerotic; antigout; antiarteriosclerotic;
KW hepatotropic; antiinflammatory; virucide; cytostatic; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200246415-A2.

XX

PD 13-JUN-2002.

XX

PF 05-DEC-2001; 2001WO-US046963.

XX

PR 08-DEC-2000; 2000US-0254303P.

PR 15-DEC-2000; 2000US-0256190P.

PR 21-DEC-2000; 2000US-0257504P.

PR 12-JAN-2001; 2001US-0261546P.

PR 19-JAN-2001; 2001US-0262832P.

PR 26-JAN-2001; 2001US-0264377P.

PR 02-FEB-2001; 2001US-0266019P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Lee EA, Baughn MR, Yue H, Ding L, Raumann BE, Hafalia AJA;

PI Khan FA, Nguyen DB, Elliott VS, Ramkumar J, Walia NK, Ison CH;

PI Lu Y, Gandhi AR, Warren BA, Duggan BM, Tribouley CM, Burford N;

PI Lu DAM, Lal PG, Yao MG, Xu Y, Bruns CM, Thangavelu K, Swarnakar A;

PI Tang YT, Azimzai Y, Thornton M, Arvizu C, Policky JL;

XX

DR WPI; 2002-519667/55.

DR P-PSDB; ABP74104.

XX

PT Novel human transporter and ion channel polypeptide, useful in diagnosis,
PT prevention or treatment of transport, neurological, muscle, immunological
PT and cell proliferative disorders.

XX

PS Claim 96; SEQ ID NO 41; 146pp + Sequence Listing; English.

XX

CC The invention relates to human transporter and ion channel polypeptide
CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-
CC ABP74127), a naturally occurring polypeptide comprising a sequence having
CC at least sequence 90 % identity to (I) or a biologically active or
CC immunogenic fragment of (I). (I) is useful for screening a compound for
CC effectiveness as an agonist or antagonist, for screening a compound that
CC specifically binds (I) or modulates the activity of (I) and for preparing
CC a polyclonal or monoclonal antibody by hybridoma technology.
CC Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for
CC screening a compound altering gene expression. (I) and (II) are useful in
CC a diagnostic tests for a condition or a disease associated with the
CC expression of TRICH in a biological sample, especially disorders selected
CC from a transport disorder such as cystic fibrosis, diabetes mellitus,
CC Parkinson's disease, cardiac disorders, neurological disorders such as
CC Alzheimer's disease, Huntington's disease, muscle disorders,
CC immunological disorder such as AIDS, asthma and atherosclerosis, and cell
CC proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and
CC cancer. (II) is useful for creating knock-in humanised animals or
CC transgenic animals to model human diseases, in somatic or germline gene

CC therapy, to generate a transcript image of a tissue or cell type, for
CC detecting differences in the chromosomal location due to translocation,
CC inversion among normal, carrier or affected individuals and for mapping
CC genomic sequences. Note: The sequence data for this patent is not
CC represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX

SQ Sequence 2966 BP; 692 A; 725 C; 809 G; 740 T; 0 U; 0 Other;

Query Match 99.9%; Score 2764.4; DB 6; Length 2966;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
      |||
Db     201 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 260

Qy      61 TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
      |||
Db     261 TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 320

Qy     121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
      |||
Db     321 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 380

Qy     181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
      |||
Db     381 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 440

Qy     241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
      |||
Db     441 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 500

Qy     301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
      |||
Db     501 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 560

Qy     361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC 420
      |||
Db     561 ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC 620

Qy     421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
      |||
Db     621 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 680

Qy     481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
      |||
Db     681 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 740

Qy     541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
      |||
Db     741 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 800

Qy     601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
      |||
Db     801 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 860
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Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	861	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	920
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	921	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	980
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	981	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1040
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1041	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1100
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1101	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1160
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1161	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1220
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1221	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1280
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1281	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1340
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1341	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1400
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1401	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1460
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1461	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1520
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1521	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1580
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1581	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1640
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1641	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1700
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560

Db	1701	 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1760
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1761	 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1820
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1821	 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1880
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1881	 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1940
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1941	 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	2000
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	2001	 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	2060
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	2061	 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	2120
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	2121	 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	2180
Qy	1981	GAAGTCATCATTGAAGAGTCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	2181	 GAAGTCATCATTGAAGAGTCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2240
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTTCATGGAGGCCATC	2100
Db	2241	 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTTCATGGAGGCCATC	2300
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2301	 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2360
Qy	2161	TGCTTTGACTACGTCATGCACTTCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2361	 TGCTTTGACTACGTCATGCACTTCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2420
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2421	 CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2480
Qy	2281	ATGCTCACC GCCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAA	2340
Db	2481	 ATGCTCACC GCCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAA	2540
Qy	2341	GATTCAAGTCACAGCTGTTGTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400

Db	2541	GATTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC	2600
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2601	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2660
Qy	2461	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2661	AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2720
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2721	TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2780
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2781	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2840
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2841	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2900
Qy	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Db	2901	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2960
Qy	2761	TTCTAA	2766
Db	2961	TTCTAA	2966

RESULT 5

ABN83428

ID ABN83428 standard; cDNA; 2782 BP.

XX

AC ABN83428;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein coding sequence.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
 KW spleen; testis; leukocyte; foetal brain; chromosome 14; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 10. .2775

FT /*tag= a

FT /product= "Human transporter"

XX

PN WO200233086-A2.

XX

PD 25-APR-2002.

XX

PF 17-OCT-2001; 2001WO-US032152.

XX

PR 17-OCT-2000; 2000US-0240836P.
PR 13-MAR-2001; 2001US-00804474.

XX

PA (PEKE) PE CORP NY.

XX

PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;
PI Beasley EM;

XX

DR WPI; 2002-479677/51.

DR P-PSDB; ABB83246.

XX

PT Human transporter peptide related to sodium/calcium exchanger subfamily
PT for identifying modulators useful for treating a disease or condition
PT mediated by human transporter protein.

XX

PS Claim 4; Fig 1; 200pp; English.

XX

CC The present sequence is the coding sequence of a human transporter
CC protein, which is related to the sodium/calcium exchanger subfamily.
CC Experimental data indicates expression of the transporter gene in humans
CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal
CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR

XX

SQ Sequence 2782 BP; 655 A; 685 C; 766 G; 676 T; 0 U; 0 Other;

Query Match 99.8%; Score 2761.2; DB 6; Length 2782;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	10	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	69
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	70	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	130	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	249
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	250	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	369
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	370	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	429

Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC	480
Db	430	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC	489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	669
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	670	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	729
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	730	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	909
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	910	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC	969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1029
Qy	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1030	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320

Db	1270	 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1330	 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1390	 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1450	 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1510	 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1570	 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1629
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1630	 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1689
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1690	 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1749
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800
Db	1750	 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1809
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1810	 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1869
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1870	 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1929
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	1930	 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1989
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2040
Db	1990	 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG	2049
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTCATGGAGGCCATC	2100
Db	2050	 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTCATGGAGGCCATC	2109
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160

Db	2110	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2169
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2170	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2229
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2230	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2289
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Db	2290	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2349
Qy	2341	GATTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2350	GATTCGGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC	2409
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2410	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2469
Qy	2461	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2470	AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2529
Qy	2521	TGGGCTCTGCAGGGACAGGAGTTCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCA	2580
Db	2530	TGGGCTCTGCAGGGACAGGAGTTCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCA	2589
Qy	2581	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGC	2640
Db	2590	CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGC	2649
Qy	2641	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGT	2700
Db	2650	CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGT	2709
Qy	2701	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGG	2760
Db	2710	AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGG	2769
Qy	2761	TTCTAA	2766
Db	2770	TTCTAA	2775

RESULT 6

ABQ78865

ID ABQ78865 standard; cDNA; 2769 BP.

XX

AC ABQ78865;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA GCA mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW gene; ss; mutant.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers
FT mutation replace(2113. .2115,-)
FT /*tag= a

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

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PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.

XX

PS Disclosure; Page; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)

XX

SQ Sequence 2769 BP; 656 A; 679 C; 761 G; 673 T; 0 U; 0 Other;

Query Match 99.5%; Score 2753; DB 6; Length 2769;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2766; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 60
|
Db 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 60

Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
|
Db 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy	121	ACAGGGCAGAACAATGAGTCCTGTT	CAGGGTCATCGGACTGCAAGGAGGGTGT	CATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTT	CAGGGTCATCGGACTGCAAGGAGGGTGT	CATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTT	CCCTTGGGGACAAGATTGCCAGGGT	CATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTT	CCCTTGGGGACAAGATTGCCAGGGT	CATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTT	CCCTTGGGGTGTCCATCATTGCT	GACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTT	CCCTTGGGGTGTCCATCATTGCT	GACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCT	CAAGAGAGGGAGGTGACAATTAAGAA	ACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCT	CAAGAGAGGGAGGTGACAATTAAGAA	ACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATT	CGGGTCTGGAATGAACTGTCTCCA	ACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATT	CGGGTCTGGAATGAACTGTCTCCA	ACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCTCTGCTCCT	GAGATACTCCTCTCTTTAATTGAGGT	GTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCTCTGCTCCT	GAGATACTCCTCTCTTTAATTGAGGT	GTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTT	CTACCATTGTAGGGAGTGCAGCCTT	CAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTT	CTACCATTGTAGGGAGTGCAGCCTT	CAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCT	ACGTGATCCCAGACGGAGAGACTCG	CAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCT	ACGTGATCCCAGACGGAGAGACTCG	CAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCT	GCCTTGGAGTATCTTTGCCTACAT	CTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCT	GCCTTGGAGTATCTTTGCCTACAT	CTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCCT	GGTGTGGTCCAGGTTTGGGAAGGCCT	CCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCCT	GGTGTGGTCCAGGTTTGGGAAGGCCT	CCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTT	CTGGCCTGGGTGGCAGATAAACGACT	GCCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTT	CTGGCCTGGGTGGCAGATAAACGACT	GCCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAG	ACAAACACCGAGGAATTATCATAG	AGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAG	ACAAACACCGAGGAATTATCATAG	AGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGAT	GGATGGGAAAATGATGAATTCCC	ATTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGAT	GGATGGGAAAATGATGAATTCCC	ATTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGA	AAGGAAGTGGATGAGTCCCGCAG	AGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGA	AAGGAAGTGGATGAGTCCCGCAG	AGAGATGATCCGGATTCTC	960

Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATT CAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATT CAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCAT AAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCAT AAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860

Db	1801	 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1861	 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	1921	 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Qy	1981	GAAGTCATCATTGAAGAGTCTTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Db	1981	 GAAGTCATCATTGAAGAGTCTTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Db	2041	 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Qy	2101	ACCGTCAGT---GCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCC	2157
Db	2101	 ACCGTCAGTGCAGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCC	2160
Qy	2158	TCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGT	2217
Db	2161	 TCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGT	2220
Qy	2218	GTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATT	2277
Db	2221	 GTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATT	2280
Qy	2278	GGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTC	2337
Db	2281	 GGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTC	2340
Qy	2338	AAAGATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTT	2397
Db	2341	 AAAGATTTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTT	2400
Qy	2398	GCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACG	2457
Db	2401	 GCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACG	2460
Qy	2458	GGCAGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATC	2517
Db	2461	 GGCAGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATC	2520
Qy	2518	TACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACACTGGCCTTCTCCGTC	2577
Db	2521	 TACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACACTGGCCTTCTCCGTC	2580
Qy	2578	ACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCG	2637
Db	2581	 ACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCG	2640
Qy	2638	CACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTT	2697

Db 2641 CACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTT 2700

Qy 2698 GTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAG 2757
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 2701 GTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAG 2760

Qy 2758 GGGTTCTAA 2766
 ||||||||

Db 2761 GGGTTCTAA 2769

RESULT 7

ABQ78866

ID ABQ78866 standard; cDNA; 2769 BP.

XX

AC ABQ78866;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA A/G+GCA mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;

KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;

KW gene; ss; mutant.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT mutation replace(1889,A)

FT /*tag= a

FT mutation replace(2113. .2115,-)

FT /*tag= b

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are

PT structurally related to mammalian sodium-calcium exchanger proteins,

PT useful for drug screening, diagnosis and in gene therapy of biological

PT disorders.

XX

PS Disclosure; Page; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),

CC that shares structural similarity with mammalian sodium-calcium exchanger

Db	601	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500

Db	1441	TTTGTAAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1861	CCGAAATGGATGGAACGTGGAATATCAGGTGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Db	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Db	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC	2100
Qy	2101	ACCGTCAGT---GCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCC	2157
Db	2101	ACCGTCAGTGCAGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCC	2160
Qy	2158	TCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGT	2217
Db	2161	TCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGT	2220
Qy	2218	GTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATT	2277
Db	2221	GTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATT	2280
Qy	2278	GGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTC	2337
Db	2281	GGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTC	2340

Qy 2338 AAAGATTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTT 2397
 |||
 Db 2341 AAAGATTCAGTCACAGCTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTT 2400
 Qy 2398 GCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACG 2457
 |||
 Db 2401 GCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACG 2460
 Qy 2458 GGCAGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATC 2517
 |||
 Db 2461 GGCAGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATC 2520
 Qy 2518 TACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTC 2577
 |||
 Db 2521 TACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTC 2580
 Qy 2578 ACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCG 2637
 |||
 Db 2581 ACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCG 2640
 Qy 2638 CACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTT 2697
 |||
 Db 2641 CACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTT 2700
 Qy 2698 GTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAG 2757
 |||
 Db 2701 GTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAG 2760
 Qy 2758 GGGTTCTAA 2766
 |||
 Db 2761 GGGTTCTAA 2769

RESULT 8

ABA04756

ID ABA04756 standard; cDNA; 2781 BP.

XX

AC ABA04756;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3, cDNA.

XX

KW Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
 KW cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
 KW myocarditis; pulmonary hypertension; cardiotoxicity; cardiant; Vaccine;
 KW coronary heart disease; renal failure; ischaemic disorder;
 KW Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .2781

FT /*tag= a

FT /partial

FT /product= "Human natrium(+)-calcium(2+) exchanger form 3

```
FT      protein, HNCX3"
FT      /note= "No stop codon given"
```

PN WO200183744-A2.

PD 08-NOV-2001.

PF 30-APR-2001; 2001WO-EP004886.

PR 02-MAY-2000; 2000EP-00109080.

PA (MERE) MERCK PATENT GMBH.

PI Wilm C;

DR WPI; 2002-041493/05.

DR P-PSDB; AAM47745.

PT New polypeptide, useful as vaccines for inducing immune response against
PT diseases such as myocardial infarction, arrhythmia, ischemic disorders,
PT renal disorders in mammal.

PS Claim 4; Page 34-38; 41pp; English.

CC The present sequence is the coding sequence for human Sodium(+)-Calcium
CC (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome
CC 14. HNCX3 and its coding sequence are useful for treating acute and
CC chronic cardiac failure of different aetiologies, myocardial infarction,
CC cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,
CC cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,
CC acute and chronic renal failure, ischaemic disorders of skeletal muscle
CC and ischaemic brain disorders of different aetiologies

SQ Sequence 2781 BP; 658 A; 678 C; 765 G; 680 T; 0 U; 0 Other;

Query Match 98.8%; Score 2733.4; DB 6; Length 2781;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2762; Conservative 0; Mismatches 1; Indels 18; Gaps 1;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Db 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
| | | | |

Db 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy 121 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 180

Db 121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

QY 181 CCAATCTGGTACCCGGAGAACCCTTCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
 ||| | | | | | | | | | | | | | | | | |

Db 181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy 241 TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
|||||

Db	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140

Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATC-----AGATGTGACAGACAGG	1902
Db	1861	CCGAAATGGATGGAACGTGGAATATCAGGTGTGAGATTCTTTAAAGATGTGACAGACAGG	1920
Qy	1903	AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG	1962
Db	1921	AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG	1980

Qy	1963	GGTGAACACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG	2022
Db	1981	GGTGAACACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG	2040
Qy	2023	GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGAC	2082
Db	2041	GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGAC	2100
Qy	2083	CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG	2142
Db	2101	CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG	2160
Qy	2143	GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG	2202
Db	2161	GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG	2220
Qy	2203	GTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC	2262
Db	2221	GTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC	2280
Qy	2263	TCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGC	2322
Db	2281	TCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGC	2340
Qy	2323	TGCACCATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTTCGTGGCATTGTCACCTCT	2382
Db	2341	TGCACCATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTTCGTGGCATTGTCACCTCT	2400
Qy	2383	GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC	2442
Db	2401	GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC	2460
Qy	2443	ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGG	2502
Db	2461	ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGG	2520
Qy	2503	TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACA	2562
Db	2521	TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACA	2580
Qy	2563	CTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG	2622
Db	2581	CTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG	2640
Qy	2623	TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC	2682
Db	2641	TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC	2700
Qy	2683	ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC	2742
Db	2701	ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC	2760
Qy	2743	TATTGCTACATCAAGGGGTTT	2763
Db	2761	TATTGCTACATCAAGGGGTTT	2781

RESULT 9

ABX56263

ID ABX56263 standard; DNA; 2685 BP.

XX

AC ABX56263;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1c 248057963 DNA SEQ ID 5.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease; ds.

XX

OS Homo sapiens.

XX

PN WO200281625-A2.

XX

PD 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-US010366.

XX

PR 03-APR-2001; 2001US-0281086P.

PR 05-APR-2001; 2001US-0281906P.

PR 06-APR-2001; 2001US-0282020P.

PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.

PR 12-APR-2001; 2001US-0283512P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285325P.

PR 20-APR-2001; 2001US-0285381P.

PR 24-APR-2001; 2001US-0286068P.

PR 25-APR-2001; 2001US-0286292P.

PR 07-JUN-2001; 2001US-0296692P.

PR 26-JUN-2001; 2001US-0300883P.

PR 08-AUG-2001; 2001US-0311003P.

PR 13-AUG-2001; 2001US-0311973P.

PR 16-AUG-2001; 2001US-0312901P.

PR 14-SEP-2001; 2001US-0322283P.

PR 05-OCT-2001; 2001US-0327448P.

PR 31-DEC-2001; 2001US-0345734P.

PR 03-JAN-2002; 2002US-0345755P.

PR 04-FEB-2002; 2002US-0354391P.

PR 02-APR-2002; 2002US-00114153.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;

PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;

PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;

PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
PI Mazur A;

XX

DR WPI; 2003-046862/04.

DR P-PSDB; ABU12043.

XX

PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.

XX

PS Claim 3; Page 85-86; 425pp; English.

XX

CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABX56261-ABX56306 represent the polynucleotide fragments
CC which encode the NOVX polypeptides represented in ABU12041-ABU12086

XX

SQ Sequence 2685 BP; 645 A; 657 C; 741 G; 642 T; 0 U; 0 Other;

Query Match 96.6%; Score 2673.2; DB 7; Length 2685;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2675; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	86	GAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTT	145
Db	2	GATCCGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTT	61
Qy	146	CAGGGTCATCGGACTGCAAGGAGGGTGTCTATCTGCCAATCTGGTACCCGGAGAACCCTT	205
Db	62	CAGGGTCATCGGACTGCAAGGAGGGTGTCTATCTGCCAATCTGGTACCCGGAGAACCCTT	121
Qy	206	CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC	265
Db	122	CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC	181
Qy	266	TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG	325
Db	182	TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG	241

Qy	326	AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTTCGGGTCT	385
Db	242	AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTTCGGGTCT	301
Qy	386	GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATAC	445
Db	302	GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATAC	361
Qy	446	TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTA	505
Db	362	TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTA	421
Qy	506	CCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGA	565
Db	422	CCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGA	481
Qy	566	TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTT	625
Db	482	TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTT	541
Qy	626	GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG	685
Db	542	GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG	601
Qy	686	TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCT	745
Db	602	TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCT	661
Qy	746	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	805
Db	662	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	721
Qy	806	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	865
Db	722	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	781
Qy	866	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG	925
Db	782	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG	841
Qy	926	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	985
Db	842	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	901
Qy	986	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAACAGA	1045
Db	902	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAACAGA	961
Qy	1046	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1105
Db	962	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1021
Qy	1106	TGAAGAAACATGCAGCAGAACCAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1165
Db	1022	TGAAGAAACATGCAGCAGAACCAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1081
Qy	1166	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1225

Db	1082	 ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1141
Qy	1226	AGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATGTCAAAGACCA	1285
Db	1142	 AGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATGTCAAAGACCA	1201
Qy	1286	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1345
Db	1202	 TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1261
Qy	1346	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1405
Db	1262	 CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1321
Qy	1406	TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1465
Db	1322	 TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1381
Qy	1466	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1525
Db	1382	 TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1441
Qy	1526	CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1585
Db	1442	 CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1501
Qy	1586	CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG	1645
Db	1502	 CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG	1561
Qy	1646	AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTTAGGACAG	1705
Db	1562	 AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTTAGGACAG	1621
Qy	1706	TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1765
Db	1622	 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1681
Qy	1766	TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACG	1825
Db	1682	 TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACG	1741
Qy	1826	AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT	1885
Db	1742	 AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT	1801
Qy	1886	CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1945
Db	1802	 CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1861
Qy	1946	TGGGAAAGCCAGTATTGGGTGAACACCCCAAAGTAGAAGTCATCATTGAAGAGTCCTATG	2005
Db	1862	 TGGGAAAGCCAGTATTGGGTGAACACCCCAAAGTAGAAGTCATCATTGAAGAGTCCTATG	1921
Qy	2006	AGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA	2065

Db	1922	AGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA	1981
Qy	2066	CCCATTCTGGAGGGACCAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGG	2125
Db	1982	CCCATTCTGGAGGGACCAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGG	2041
Qy	2126	ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC	2185
Db	2042	ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC	2101
Qy	2186	TGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCT	2245
Db	2102	TGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCT	2161
Qy	2246	GGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACC	2305
Db	2162	GGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACC	2221
Qy	2306	TGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAAGATTAGTACAGCTGTTGTTTTTCG	2365
Db	2222	TGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAAGATTAGTACAGCTGTTGTTTTTCG	2281
Qy	2366	TGGCATTGTCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATG	2425
Db	2282	TGGCATTGTCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATG	2341
Qy	2426	TATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGG	2485
Db	2342	TATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGG	2401
Qy	2486	GCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCC	2545
Db	2402	GCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCC	2461
Qy	2546	ACGTGTCGGCCGGCACACTGGCCTTCTCCGTACCCTCTTCACCATCTTTGCATTTGTCT	2605
Db	2462	ACGTGTCGGCCGGCACACTGGCCTTCTCCGTACCCTCTTCACCATCTTTGCATTTGTCT	2521
Qy	2606	GCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCC	2665
Db	2522	GCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCC	2581
Qy	2666	GTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCT	2725
Db	2582	GTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCT	2641
Qy	2726	TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC	2763
Db	2642	TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC	2679

RESULT 10

ABX56262

ID ABX56262 standard; DNA; 2840 BP.

XX

AC ABX56262;

XX

DT 19-FEB-2003 (first entry)
 XX
 DE Human NOV1b CG56558-02 DNA SEQ ID 3.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200281625-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010366.
 XX
 PR 03-APR-2001; 2001US-0281086P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 06-APR-2001; 2001US-0282020P.
 PR 10-APR-2001; 2001US-0282930P.
 PR 12-APR-2001; 2001US-0283444P.
 PR 12-APR-2001; 2001US-0283512P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285381P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 25-APR-2001; 2001US-0286292P.
 PR 07-JUN-2001; 2001US-0296692P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 08-AUG-2001; 2001US-0311003P.
 PR 13-AUG-2001; 2001US-0311973P.
 PR 16-AUG-2001; 2001US-0312901P.
 PR 14-SEP-2001; 2001US-0322283P.
 PR 05-OCT-2001; 2001US-0327448P.
 PR 31-DEC-2001; 2001US-0345734P.
 PR 03-JAN-2002; 2002US-0345755P.
 PR 04-FEB-2002; 2002US-0354391P.
 PR 02-APR-2002; 2002US-00114153.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
 PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
 PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
 PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
 PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
 PI Mazur A;
 XX
 DR WPI; 2003-046862/04.
 DR P-PSDB; ABU12042.

XX
PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.

Db	363	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	422
Qy	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	423	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	482
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	483	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	542
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	543	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	602
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	603	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	662
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	663	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	722
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	723	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	782
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	783	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	842
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	843	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	902
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	903	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	962
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	963	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1022
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1023	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1082
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1083	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1142
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1143	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1202
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1203	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1262

Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1263	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1322
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1323	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1382
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1383	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1442
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1443	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1502
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1503	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1562
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1563	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1622
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1623	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1682
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1683	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1742
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1743	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1802
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAGGGTT	1800
Db	1803	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACAATTACATC	1862
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1863	AAGGTAATTGATGATGAGGCATATGAGAAAAACAAGAATTACTTCATTGAGATGATGGGC	1922
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTG-----ACAGACAGGAAGCTG	1908
Db	1923	CCCCGCATGGTGGATATGAGTTTTTCAGAAAGCGCTCCTGTTATCTCCAGACAGGAAGCTG	1982
Qy	1909	ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA	1968
Db	1983	ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA	2042
Qy	1969	CACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAA	2028
Db	2043	CACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAA	2102

Qy	2029	CTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTC	2088
Db	2103	CTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTC	2162
Qy	2089	ATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAG	2148
Db	2163	ATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAG	2222
Qy	2149	AGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCTGACTGTCTTCTGGAAGGTGCTG	2208
Db	2223	AGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCTGACTGTCTTCTGGAAGGTGCTG	2282
Qy	2209	TTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATC	2268
Db	2283	TTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATC	2342
Qy	2269	CTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACC	2328
Db	2343	CTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACC	2402
Qy	2329	ATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTCGTGGCATTGGGCACCTCTGTCCCA	2388
Db	2403	ATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTCGTGGCATTGGGCACCTCTGTCCCA	2462
Qy	2389	GATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGC	2448
Db	2463	GATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGC	2522
Qy	2449	AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG	2508
Db	2523	AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG	2582
Qy	2509	GCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCC	2568
Db	2583	GCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCC	2642
Qy	2569	TTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGA	2628
Db	2643	TTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGA	2702
Qy	2629	AGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACA	2688
Db	2703	AGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACA	2762
Qy	2689	TGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGC	2748
Db	2763	TGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGC	2822
Qy	2749	TACATCAAGGGGTTCTAA	2766
Db	2823	TACATCAAGGGGTTCTAA	2840

RESULT 11

ABX56261

ID ABX56261 standard; DNA; 2813 BP.

XX

AC ABX56261;
 XX
 DT 19-FEB-2003 (first entry)
 XX
 DE Human NOV1a CG56258-01 DNA SEQ ID 1.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200281625-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010366.
 XX
 PR 03-APR-2001; 2001US-0281086P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 06-APR-2001; 2001US-0282020P.
 PR 10-APR-2001; 2001US-0282930P.
 PR 12-APR-2001; 2001US-0283444P.
 PR 12-APR-2001; 2001US-0283512P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285381P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 25-APR-2001; 2001US-0286292P.
 PR 07-JUN-2001; 2001US-0296692P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 08-AUG-2001; 2001US-0311003P.
 PR 13-AUG-2001; 2001US-0311973P.
 PR 16-AUG-2001; 2001US-0312901P.
 PR 14-SEP-2001; 2001US-0322283P.
 PR 05-OCT-2001; 2001US-0327448P.
 PR 31-DEC-2001; 2001US-0345734P.
 PR 03-JAN-2002; 2002US-0345755P.
 PR 04-FEB-2002; 2002US-0354391P.
 PR 02-APR-2002; 2002US-00114153.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
 PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
 PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
 PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
 PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
 PI Mazur A;
 XX

Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	309	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	368
Qy	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	369	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	428
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	429	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	488
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	489	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	548
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	549	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	608
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	609	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	668
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	669	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	728
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	729	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	788
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	789	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	848
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	849	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	908
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	909	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	968
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	969	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1028
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1029	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1088
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1089	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1148
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200

Db	1149	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1208
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1209	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1268
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1269	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1328
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ID ACC00414 standard; cDNA; 2534 BP.
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 AC ACC00414;
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 DT 04-JUL-2003 (first entry)
 XX
 DE Human 69039 coding sequence.
 XX
 KW Human; 69039; neuroprotective; gene therapy; haematopoietic disorder;
 KW Na+/Ca2+ exchanger; ion transporter; neural tissue;
 KW neurological disorder; gene; ss.
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 OS Homo sapiens.
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 PD 10-APR-2003.
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 PF 27-SEP-2002; 2002WO-US030817.
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 PR 28-SEP-2001; 2001US-0325737P.
 XX
 PA (MILL-) MILLENIUM PHARM INC.
 XX
 PI Carroll JM;
 XX
 DR WPI; 2003-381617/36.
 DR P-PSDB; ABR40134.
 XX
 PT Identifying a nucleic acid molecule associated with a disorder for
 PT preparing a composition for treating hematopoietic or neurological
 PT disorder by detecting the presence of a nucleic acid molecule in the
 PT sample that is amplified.
 XX
 PS Claim 1; Page 109-110; 133pp; English.
 XX
 CC The present sequence is the coding sequence for human 69039, a novel
 CC Na+/Ca2+ exchanger family member (ion transporter). 69039 was shown to be
 CC expressed in human haematopoietic cells, e.g. CD34-expressing progenitor
 CC cells as well as in neural tissues, e.g. brain cortex and hypothalamus.
 CC 69039 may therefore be used for preparing a composition for treating
 CC haematopoietic or neurological disorder
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 SQ Sequence 2534 BP; 602 A; 595 C; 644 G; 693 T; 0 U; 0 Other;

 Query Match 64.6%; Score 1786.4; DB 7; Length 2534;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
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Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
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Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
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Db	1903	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1962
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1963	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	2022
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2023	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2082
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAA	1788

Db 2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGTAA 2130

RESULT 13

ABN83429

ID ABN83429 standard; DNA; 126512 BP.

XX

AC ABN83429;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein gene.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;

KW spleen; testis; leukocyte; foetal brain; chromosome 14; gene;

KW single nucleotide polymorphism; SNP; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

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Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	2550	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	2609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	2610	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	2669
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	2670	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	2729
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	2730	 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	2789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	2790	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	2849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	2850	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	2909
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	2910	 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	2969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	2970	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	3029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	3030	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	3089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140

Db	3090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	3149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	3150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	3209
Qy	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	3210	GACCCATGTTCTTACCAAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	3269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	3270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	3329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	3330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	3389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	3390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	3449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	3450	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	3509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	3510	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	3569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	3570	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	3629
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	3630	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	3689
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	3690	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	3749
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAA	1788
Db	3750	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGTAA	3797

RESULT 14

ABQ78862

ID ABQ78862 standard; cDNA; 1863 BP.

XX

AC ABQ78862;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #2 cDNA.

XX

Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACTACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	361	ACCAGCACAACTACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020

Db	961	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCAGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCAGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG	1796
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Qy	1797	GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA	1837

Db 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841

RESULT 15

AAH57377

ID AAH57377 standard; cDNA; 2814 BP.

XX

AC AAH57377;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human heart cell specific cDNA sequence SEQ ID NO:217.

XX

KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;

KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;

KW metabolic disease; developmental disease; cytostatic; immunomodulatory;

KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

XX

OS Homo sapiens.

XX

PN WO200132927-A2.

XX

PD 10-MAY-2001.

XX

PF 02-NOV-2000; 2000WO-US030396.

XX

PR 04-NOV-1999; 99US-0163508P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Sornasse T, Seilhamer JJ, Watson GA;

XX

DR WPI; 2001-291057/30.

XX

PT New cell and tissue specific polynucleotides useful for diagnosis,
PT prognosis or monitoring of treatments for disorders where the gene is
PT associated with a cancer, immunopathology or neuropathology.

XX

PS Claim 1; Page 146-147; 327pp; English.

XX

CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC sequences (I). (I) can have cytostatic, immunomodulatory and
CC neuroprotective activities, and can be used in gene therapy. (I) and
CC proteins (II) encoded by then are used in high throughput screening
CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their
CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
CC agents. Expression of (I) in a sample indicates the differentiation of
CC embryonic stem cells into a tissue selected from brain, heart, kidney,
CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
CC to produce an expression profile that defines a metabolic or
CC developmental process, treatment, condition, disease or disorder. The
CC gene profile can be used for diagnosis, prognosis or monitoring of
CC treatments and for investigating a predisposition to a disorder where the
CC gene is associated with a cancer, immunopathology or neuropathology

XX

SQ Sequence 2814 BP; 754 A; 579 C; 718 G; 763 T; 0 U; 0 Other;

Query Match 48.0%; Score 1326.4; DB 4; Length 2814;
 Best Local Similarity 69.8%; Pred. No. 0;
 Matches 1893; Conservative 0; Mismatches 756; Indels 63; Gaps 5;

Qy	109	GACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAG	168
Db	112	GAAATGGAAGGAGAAGGAAATGAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA	171
Qy	169	GGTGTATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG	228
Db	172	GGGGTGATTTTGCCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA	231
Qy	229	GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGAC	288
Db	232	GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT	291
Qy	289	CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA	348
Db	292	CGGTTTCATGTCCTCTATAGAAGTCATCACATCTCAAGAAAAGAAATAACCATAAAGAAA	351
Qy	349	CCCAATGGAGAAACCAGCACAAACCCTATTTCGGGTCTGGAATGAACTGTCTCCAACCTG	408
Db	352	CCCAATGGAGAGACCACCAAGACAACCTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG	411
Qy	409	ACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT	468
Db	412	ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTCAGTAATTGAAGTGTGT	471
Qy	469	GGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC	528
Db	472	GGCCATAACTTCACTGCAGGAGACCTCGGTCTAGCACCATCGTGGGAAGTGTGCATTTC	531
Qy	529	AACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG	588
Db	532	AATATGTTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG	591
Qy	589	ATCAAGCATCTACGAGTCTTCTTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG	648
Db	592	ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG	651
Qy	649	CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC	708
Db	652	CTTTACATTATTTTGTCTGTATATCTCCTGGTGTGTGGAGGTCTGGGAAGGTTTGCTT	711
Qy	709	ACTCTCTTCTTCTTTCCAGTGTGTGCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC	768
Db	712	ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTTCGCTTGGGTAGCGGATAGGAGACTTCTG	771
Qy	769	TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG	828
Db	772	TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA	831
Qy	829	ACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATGAAT	879
Db	832	CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT	891

Qy	880	TCCCATTTTCTAGATGGGAACCTGGTGCCCTGGGAAGGGAAG-----	921
Db	892	TCTCATGTTGAAAATTTCTTAGATGGTGCTCTGGTTCCTGGAGGTGGATGAGAGGGACCAA	951
Qy	922	GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC	981
Db	952	GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACTTAAGCAGAAGCAT	1011
Qy	982	CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAA	1041
Db	1012	CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG	1071
Qy	1042	CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT	1101
Db	1072	CAAAAAAGTAGAGCATTTTATCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC	1131
Qy	1102	ATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC	1161
Db	1132	ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCAGCATGCACGAGGTCAAC	1191
Qy	1162	ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG	1218
Db	1192	ACTGAAGTGACTGAAAATGACCCTGTTAGTAAGATCTTCTTTGAACAAGGGACATATCAG	1251
Qy	1219	TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCA	1278
Db	1252	TGTCTGGAGAACTGTGGTACTGTGGCCCTTACCATTATCCGCAGAGGTGGTGATTTGACT	1311
Qy	1279	AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT	1338
Db	1312	AACACTGTGTTTGTTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT	1371
Qy	1339	GAGTTCACAGAGGGGCACGGTGGTTCCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG	1398
Db	1372	GAATTTACTGAAGGAAGTGTGGTGTTTAAGCCTGGTGATACCAGAAGGAAATCAGAGTG	1431
Qy	1399	GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT	1458
Db	1432	GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTCCTTGTGCATCTCAGCAAT	1491
Qy	1459	GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT	1518
Db	1492	GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC-----CAATCAT	1542
Qy	1519	CCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGAT	1578
Db	1543	GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACATATTTTGGATGAT	1602
Qy	1579	GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGT	1638
Db	1603	GACCACGCAGGCATTTTACTTTTGAGGAACCTGTGACTCATGTGAGTGAGAGCATTGGC	1662
Qy	1639	GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTT	1698
Db	1663	ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT	1722
Qy	1699	AGGACAGTAGAAGGGACAGCCAAGGTTGGCGGTGAGGACTTTGAAGACACATATGGGGAG	1758

Db	1723	AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTTGAGGACACTTGTGGAGAG	1782
Qy	1759	TTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAG	1818
Db	1783	CTCGAATTCCAGAATGATGAAATTGTGAAGATCATTACCATTAGAATATTTGACCGTGAG	1842
Qy	1819	GAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGT	1878
Db	1843	GAATATGAGAAAGAGTGCAGTTTCTCCCTTGTGCTTGAGGAACCAAATGGATAAGAAGA	1902
Qy	1879	GGAATATCAG-----ATGTGACAGACAGGAAGCTGACTATG	1914
Db	1903	GGAATGAAAGGTGGCTTCACAATAACAGACGAATATGATGACAAGCAGCCACTGACCAGC	1962
Qy	1915	GAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCC	1974
Db	1963	AAAGAGGAAGAGGAGAGGCGCATTGCAGAAATGGGGCGCCCCATCCTGGGAGAGCACACC	2022
Qy	1975	AACTAGAAAGTCATCATTGAAGAGTCTATGAGTTCAAGACTACGGTGGACAAACTGATC	2034
Db	2023	AAGTTGGAAGTGATCATTGAAGAATCCTATGAATTCAGAGTACTGTGGACAAACTCATT	2082
Qy	2035	AAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAG	2094
Db	2083	AAGAAGACAAACCTGGCCTTGTGGTTGGGACTAACAGCTGGAGAGAACAGTTCATTGAA	2142
Qy	2095	GCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTG	2154
Db	2143	GCTATCACTGTCAGTGCTGGGGAAGATGATGACGACGATGAATGTGGGAAGAGAAGCTG	2202
Qy	2155	CCCTCCTGCTTTGACTACGTGCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCC	2214
Db	2203	CCCTCCTGTTTCGATTACGTGATGCACTTTCTGACTGTGTTCTGGAAGGTCCTGTTTGCC	2262
Qy	2215	TGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATC	2274
Db	2263	TTCGTCCCCCTACTGAATACTGGAATGGCTGGGCGTGTTTCATTGTCTCCATCCTCATG	2322
Qy	2275	ATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGT	2334
Db	2323	ATTGGCCTACTGACAGCTTTCATTGGAGACCTGGCTTCCCACTTTGGCTGCACCATTGGC	2382
Qy	2335	CTCAAAGATTCACTCACAGCTGTTGTTTTCTGTTGGCATTGGCACCTCTGTCCCAGATACG	2394
Db	2383	CTGAAAGATTCTGTGACTGCAGTCGTGTTTCGTGCGCACTTGGAACATCAGTGCCAGACACA	2442
Qy	2395	TTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTG	2454
Db	2443	TTTGCCAGCAAAGTGGCAGCCACCCAGGACCAGTATGCAGACGCCTCCATAGGTAACGTC	2502
Qy	2455	ACGGGCAGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCC	2514
Db	2503	ACGGGCAGCAACGCCGTGAATGTCTTCTGGGAATCGGTGTGGCCTGGTCCATCGCTGCC	2562
Qy	2515	ATCTACTGGGCTCTGCAGGGACAGGAGTTCACGTGTGCGCCGGCACACTGGCCTTCTCC	2574

Db 2563 ATCTACCACGCAGCCAATGGGGAACAGTTCAAAGTGTCCCCTGGCACAAGCTTTCTCT 2622
 Qy 2575 GTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGG 2634
 ||||| ||||| ||||| || || | ||||| ||||| || ||
 Db 2623 GTCACCTCTCTTCACCATTTTTGCTTTCATCAATGTGGGGGTGCTGCTGTATCGGCGGAGG 2682
 Qy 2635 CCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTC 2694
 || | | ||||| ||||| ||||| ||||| ||||| ||||| || || ||
 Db 2683 CCAGAAATCGGAGGTGAGCTGGGTGGGCCCCGGACTGCCAAGCTCCTCACATCCTGCCTC 2742
 Qy 2695 TTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATC 2754
 ||||| ||| ||||| | ||||| |||| | | || ||||| || ||||
 Db 2743 TTTGTGCTCCTATGGCTCTTGTACATTTTCTTCTCCTCCCTGGAGGCCTACTGCCACATA 2802
 Qy 2755 AAGGGGTTCTAA 2766
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 Db 2803 AAAGGCTTCTAA 2814

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY_NUC
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Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
c	1	78.8	2.8	7218	1	US-08-232-463-14		Sequence 14, Appl	
	2	76.6	2.8	1935	4	US-09-701-068-3		Sequence 3, Appli	
	3	76.6	2.8	1950	4	US-09-701-068-1		Sequence 1, Appli	
	4	51.6	1.9	7218	1	US-08-232-463-14		Sequence 14, Appl	
c	5	50.2	1.8	390	3	US-09-197-649-7		Sequence 7, Appli	
	6	46.2	1.7	3984	4	US-09-016-434-1199		Sequence 1199, Ap	
	7	46.2	1.7	4559	4	US-09-919-172-61		Sequence 61, Appl	
	8	44.8	1.6	2803	4	US-09-701-068-4		Sequence 4, Appli	
c	9	44.2	1.6	4403765	3	US-09-103-840A-2		Sequence 2, Appli	
c	10	43.8	1.6	1992	4	US-09-252-991A-9693		Sequence 9693, Ap	
	11	43.8	1.6	2658	4	US-09-252-991A-9558		Sequence 9558, Ap	

	12	43.8	1.6	2799	4	US-09-252-991A-9604	Sequence 9604, Ap
c	13	43.4	1.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	14	42.2	1.5	660	4	US-09-252-991A-5866	Sequence 5866, Ap
	15	42.2	1.5	1983	4	US-09-252-991A-5825	Sequence 5825, Ap
c	16	42.2	1.5	1995	4	US-09-252-991A-5783	Sequence 5783, Ap
	17	41.8	1.5	870	4	US-09-252-991A-3650	Sequence 3650, Ap
	18	41.8	1.5	1098	4	US-09-252-991A-3605	Sequence 3605, Ap
c	19	41.8	1.5	3402	4	US-09-252-991A-1374	Sequence 1374, Ap
	20	41.8	1.5	3687	4	US-09-252-991A-1193	Sequence 1193, Ap
	21	41.8	1.5	4266	4	US-09-252-991A-1234	Sequence 1234, Ap
	22	41.4	1.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	23	41.4	1.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	24	40.2	1.5	1174	3	US-09-034-985-1	Sequence 1, Appli
	25	40	1.4	570	4	US-09-252-991A-10419	Sequence 10419, A
c	26	40	1.4	789	4	US-09-252-991A-10654	Sequence 10654, A
c	27	40	1.4	813	4	US-09-252-991A-10547	Sequence 10547, A
	28	40	1.4	831	4	US-09-252-991A-10512	Sequence 10512, A
	29	39.6	1.4	3431	4	US-09-221-017B-993	Sequence 993, App
	30	39.2	1.4	333	4	US-09-252-991A-3700	Sequence 3700, Ap
c	31	39	1.4	642	4	US-09-252-991A-4949	Sequence 4949, Ap
	32	39	1.4	1617	4	US-09-489-039A-2262	Sequence 2262, Ap
	33	39	1.4	1926	4	US-09-249-585A-4	Sequence 4, Appli
	34	39	1.4	1931	2	US-09-130-114-2	Sequence 2, Appli
	35	39	1.4	1932	4	US-09-252-991A-4998	Sequence 4998, Ap
c	36	38.6	1.4	1548	2	US-08-762-106-5	Sequence 5, Appli
c	37	38.6	1.4	1548	3	US-09-320-774-5	Sequence 5, Appli
c	38	38.6	1.4	1581	2	US-08-762-106-6	Sequence 6, Appli
c	39	38.6	1.4	1581	3	US-09-320-774-6	Sequence 6, Appli
	40	38.4	1.4	318	4	US-09-252-991A-10314	Sequence 10314, A
	41	38.4	1.4	387	4	US-09-252-991A-1461	Sequence 1461, Ap
	42	38.4	1.4	1272	4	US-09-252-991A-1552	Sequence 1552, Ap
c	43	38.4	1.4	2777	4	US-09-310-463-3	Sequence 3, Appli
c	44	38.4	1.4	2777	4	US-08-842-248A-3	Sequence 3, Appli
	45	38.4	1.4	50937	3	US-09-428-517-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-232-463-14/c

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

```

```

Query Match          2.8%; Score 78.8; DB 1; Length 7218;
Best Local Similarity 3.8%; Pred. No. 1.7e-12;
Matches 14; Conservative 231; Mismatches 123; Indels 0; Gaps 0;

```

```

Qy      1678 GGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGAC 1737
          | || || || |      ||| | ||:: ::::: : : : : : : : : :
Db      1460 GTTAAAGAGATAGAAGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1401

Qy      1738 TTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGG 1797
          ::::: : : : : : : : : : : : : : : : : : : : : : : :
Db      1400 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1341

Qy      1798 GTTAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGT 1857
          : : : : : : : : : : : : : : : : : : : : : : : :
Db      1340 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1281

Qy      1858 GAACCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAA 1917
          ::: : : : : : : : : : : : : : : : : : : : : : : :
Db      1280 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1221

Qy      1918 GAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAA 1977
          ::::: : : : : : : : : : : : : : : : : : : : : :
Db      1220 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1161

Qy      1978 CTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAG 2037
          ::::: : : : : : : : : : : : : : : : : : : : :

```


RESULT 3

US-09-701-068-1

; Sequence 1, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-701-068-1

Query Match 2.8%; Score 76.6; DB 4; Length 1950;
Best Local Similarity 51.3%; Pred. No. 3.2e-12;
Matches 178; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

Qy	2174	TCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGT	2233
Db	1174	TCTGGCATTACTCCTCGCCCCTTGGAAGTCTTTTGCATTTGTGCCCCCTGCAACA	1233
Qy	2234	ACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCA	2293
Db	1234	TTGCTCACGGTTGGATCGCTTTCATCTGCTCTCTCCTCTTCATCAGTGGAGTAGCCTTTG	1293
Qy	2294	TCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAAAGATTAGTCACAG	2353
Db	1294	TTGTCACAAGATTTACTGACCTTATAAGCTGTGTCACTGGAATAAACCCATATGTGATAG	1353
Qy	2354	CTGTTGTTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTG	2413
Db	1354	CATTACAGCACTCGCAAGTGAAGTTCATGGCCAGACTTAGTAGCAAGTAAATCGCTG	1413
Qy	2414	CCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCA	2473
Db	1414	CAGAGCGACAATAACCGCAGATTAGCTATTGCAAACATCACCTGCAGTAACTCGGTGA	1473
Qy	2474	ATGTCTTCTCGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	1474	ACATCTATGTGGGGATTGGAGTTCGGTGGCTGATAAACACAGTCTAC	1520

RESULT 4

US-08-232-463-14

; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.


```

; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

```

```

Query Match          1.9%; Score 51.6; DB 1; Length 7218;
Best Local Similarity 5.9%; Pred. No. 0.00023;
Matches 24; Conservative 215; Mismatches 169; Indels 0; Gaps 0;

```

```

Qy      395 CTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCCTCTCTT 454
      :: :::::  ::  :::::  :  ::::  :::::  :::::  :  :::::  :::
Db      1078 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1137

Qy      455 TAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAG 514
      :  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      1138 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1197

Qy      515 GGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACG 574
      :  :  :::::  :  :  ::  :  :  :  :  :  :  :  :  :  :  :  :

```

```

Db      1198 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1257
Qy      575 GAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCT 634
          ::: :      : : : : : : : : : : : : : : : : : : : : : : : :
Db      1258 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1317
Qy      635 TTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTT 694
          :: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1318 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1377
Qy      695 GGGAAGGCCTCCTCACTCTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAG 754
          : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1378 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTA 1437
Qy      755 ATAAACGACTGCTCTTCTACAAATACATGCACAAAAGTACCGCACAG 802
          ||| | | | | | | | | | | | | | | | | | | | | |
Db      1438 CCAAATTCTTCTATCTCTTTAACTACTTGCATAGATAGGTAATTACAG 1485

```

RESULT 5

US-09-197-649-7/c

; Sequence 7, Application US/09197649

; Patent No. 6194550

; GENERAL INFORMATION:

; APPLICANT: Gold, Larry

; APPLICANT: Tuerk, Craig

; APPLICANT: Pribnow, David

; APPLICANT: Smith, Jonathan D.

; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation

; FILE REFERENCE: NEX02/C1-CON

; CURRENT APPLICATION NUMBER: US/09/197,649

; CURRENT FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: 07/829,461

; EARLIER FILING DATE: 1992-01-31

; EARLIER APPLICATION NUMBER: 07/739,055

; EARLIER FILING DATE: 1991-08-01

; EARLIER APPLICATION NUMBER: 07/561,968

; EARLIER FILING DATE: 1990-08-02

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 390

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Sequence

; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed

; OTHER INFORMATION: fragments having NcoI restriction sites.

US-09-197-649-7

Query Match 1.8%; Score 50.2; DB 3; Length 390;

Best Local Similarity 46.0%; Pred. No. 8.4e-05;

Matches 169; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

```

Qy      2238 CCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCAT 2297
          ||| ||| | | | ||| |||| | || | | | | | | | | | | | |
Db      375 CCATGGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 316

```

ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1199:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3984 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: g181907
 US-09-016-434-1199

Query Match 1.7%; Score 46.2; DB 4; Length 3984;
 Best Local Similarity 51.7%; Pred. No. 0.0065;
 Matches 105; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

```

Qy      2434 GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGC 2493
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      674 GCCTTCTCCAAGGACATCTTCTCCGTCACTTCTTCAGCTTCTTCAACTGGCTCTGC 733

Qy      2494 CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCTG 2553
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      734 GTGGCCCTGGCCATCATCGGCATGATCTGGCTGCGCCACAGAAAGCCTGAGCTTGAGCGG 793

Qy      2554 GCCGGCACACTGGCCTTCTCCGTCAACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      794 CCCATCAAGGTGAACCTGGCCCTGCCTGTGTTCTTCATCCTGGCCTGCCTCTTCCTGATC 853

Qy      2614 GTGCTCTTGTACCGAAGGCGGCC 2636
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      854 GCCGTCTCCTTCTGGAAGACACC 876
  
```

RESULT 7

US-09-919-172-61
 ; Sequence 61, Application US/09919172
 ; Patent No. 6673545
 ; GENERAL INFORMATION:
 ; APPLICANT: Faris, Mary
 ; APPLICANT: Turner, Christopher M.
 ; TITLE OF INVENTION: PROSTATE CANCER MARKERS
 ; FILE REFERENCE: PA-0036 US
 ; CURRENT APPLICATION NUMBER: US/09/919,172
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/222,469
 ; PRIOR FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 61
 ; LENGTH: 4559
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 008942.10
US-09-919-172-61

Query Match 1.7%; Score 46.2; DB 4; Length 4559;
Best Local Similarity 51.7%; Pred. No. 0.0071;
Matches 105; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

```
Qy      2434 GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCTGGGCATCGGC 2493
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1233 GCCTTCTCCAAGGACATCTTCTCCGTCATCAACTTCTTCAGCTTCTTCAACTGGCTCTGC 1292

Qy      2494 CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCG 2553
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1293 GTGGCCCTGGCCATCATCGGCATGATCTGGCTGCGCCACAGAAAGCCTGAGCTTGAGCGG 1352

Qy      2554 GCCGGCACACTGGCCTTCTCCGTACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1353 CCCATCAAGGTGAACCTGGCCCTGCCTGTGTTCTTCATCCTGGCCTGCCTCTTCCTGATC 1412

Qy      2614 GTGCTCTTGTACCGAAGGCGGCC 2636
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1413 GCCGTCTCCTTCTGGAAGACACC 1435
```

RESULT 8

US-09-701-068-4

; Sequence 4, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg²⁺/H⁺ OR Zn²⁺/H⁺ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2803
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-701-068-4

Query Match 1.6%; Score 44.8; DB 4; Length 2803;
Best Local Similarity 52.1%; Pred. No. 0.013;
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

```
Qy      477 GTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTT 536
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      950 GTTTTGTCATATAGGTCTTGGTCCTGGAACACTTGTTGGCTCAGCTGCATTTGATCTTTT 1009

Qy      537 CATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCA 596
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1010 CCCCATCCACGCTGTTTGTGTCTGTTGTGCCAAAAGCTGGAGAAGTAAAAAGATATCCGA 1069
```

Qy 597 TCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATAT 656
 || || | | | | | | | | | | | | | | | | | |
 Db 1070 CTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTTGGGCTTACATCTGGCTATACAT 1129
 Qy 657 GATTCTGGCAGT 668
 || || | ||
 Db 1130 AATCCTCGAGGT 1141

RESULT 9

US-09-103-840A-2/c

; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

Query Match 1.6%; Score 44.2; DB 3; Length 4403765;
 Best Local Similarity 46.3%; Pred. No. 3;
 Matches 145; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

Qy 2213 CCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCA 2272
 ||| | || | | | | | | | | | | | | | |
 Db 3929402 CCTCCCTTACCGCCGTTGCCGCCGGCGCCGGCGCCGGCTACGCCGCTGCCGAATCCC
 3929343
 Qy 2273 TCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTG 2332
 | | | | | | | | | | | | | | | | | | | |
 Db 3929342 GCGCCGCCGCCTTCGCCGCCGTCACCGCCTTGGCCGCCGGCGCCGCCCTCG
 3929283
 Qy 2333 GTCTCAAAGATTCAAGTACAGCTGTTGTTTTCTGGCATTGTCACCTCTGTCCCAGATA 2392
 || | | | | | | | | | | | | | | | | | |
 Db 3929282 CTCGCCACGCCTGTCGTTCCGTTCTGGCCGTACCAACCGCCCCGCCGGTGCCGCCGGTG
 3929223
 Qy 2393 CGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACG 2452
 | | | | | | | | | | | | | | | | | |

Db 3929222 CCGCCGGCCCCGTTGATGCCGCCGGCGCCGGCGTTGCCGCCGGCCCCGCCTTGGCCGCCT
3929163

Qy 2453 TGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCG 2512
| | | | | | | | | | | | | | | | | | | | | |

Db 3929162 TGGCCGCCGGCGAAGCCGTTGCCGTCTTGGGAGAGGGCGCCGCTGTCGCCGGCCCCGCCG
3929103

Qy 2513 CCATCTACTGGGC 2525
| | | | |

Db 3929102 TCGCCGCCGCGGC 3929090

RESULT 10

US-09-252-991A-9693/c

; Sequence 9693, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 9693

; LENGTH: 1992

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-9693

Query Match 1.6%; Score 43.8; DB 4; Length 1992;

Best Local Similarity 47.5%; Pred. No. 0.021;

Matches 162; Conservative 0; Mismatches 177; Indels 2; Gaps 1;

Qy 2372 TTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATG 2431
| | | | | | | | | | | | | | | | | | | | | |

Db 738 TTGGCACAGCTCGGCCTGTTCCGCCTGCTCGCCACGCTGCTGCC--GCCGGACGTACCAG 681

Qy 2432 CAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCG 2491
| | | | | | | | | | | | | | | | | | | | | |

Db 680 CCGGCGGCCTGTTCCCCGCCTTCGCCGGGGTCGCCACCGGCCTGGTATCGCTGGCCGGCT 621

Qy 2492 GCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGT 2551
| | | | | | | | | | | | | | | | | | | | | |

Db 620 TCGCCCTCCCGCCGCTGGCAGCCCTGGGCCGGGTACCGCCGTTGCGGGTCTGCGCAGCG 561

Qy 2552 CGGCCGGCACACTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCA 2611
| | | | | | | | | | | | | | | | | | | | | |

Db 560 ACCTGCTGCCGGTGCCGATGCGCACCTGGATGGCCTACGCCTGCGCCCTGCTCGCCCTGG 501

Qy 2612 GCGTGCTCTTGTACCGAAGGCGGCCGACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCT 2671

```

      || || || || | | | | || | | | |
Db      500 GCCTGATCATGTGGCGGTTGAGTCTCGACCTGAAGCTGACCCTCGCCCTGCTCGGCGGCG 441

Qy      2672 GCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTC 2712
      || | ||||| | | | | | | | |
Db      440 GCCTGGTCGCCACGCTGGTGCTCGGCGCCCTCCTGCTGCTC 400

```

RESULT 11

US-09-252-991A-9558

; Sequence 9558, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 9558

; LENGTH: 2658

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-9558

Query Match 1.6%; Score 43.8; DB 4; Length 2658;

Best Local Similarity 47.5%; Pred. No. 0.026;

Matches 162; Conservative 0; Mismatches 177; Indels 2; Gaps 1;

```

Qy      2372 TTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATG 2431
      ||||| | | | | | | | | | | | | | |
Db      1007 TTGGCACAGCTCGGCCTGTTCCGCCTGCTCGCCACGCTGCTGCC--GCCGGACGTACCAG 1064

Qy      2432 CAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCTGGGCATCG 2491
      | | | | | | | | | | | | | | | |
Db      1065 CCGGCGGCCTGTTCCCGCCTTCGCCGGGGTCGCCACCGGCCTGGTATCGCTGGCCGGCT 1124

Qy      2492 GCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGT 2551
      | | | | | | | | | | | | | | | |
Db      1125 TCGCCCTCCCGCCGCTGGCAGCCCTGGGCCGGGTACCGCCGTTGCGGGTCCTGCGCAGCG 1184

Qy      2552 CGGCCGGCACACTGGCCTTCTCCGTCACCCTCTTACCATCTTTGCATTTGTCTGCATCA 2611
      | | | | | | | | | | | | | | | |
Db      1185 ACCTGCTGCCGGTGCCGATGCGCACCTGGATGGCCTACGCCTGCGCCCTGCTCGCCCTGG 1244

Qy      2612 GCGTGCTCTTGTACCGAAGGCGGCCGACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCT 2671
      || || || || | | | | | | | | | |
Db      1245 GCCTGATCATGTGGCGGTTGAGTCTCGACCTGAAGCTGACCCTCGCCCTGCTCGGCGGCG 1304

Qy      2672 GCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTC 2712
      || | ||||| | | | | | | |

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Db 1305 GCCTGGTCGCCACGCTGGTGCTCGGCGCCCTCCTGCTGCTC 1345

RESULT 12

US-09-252-991A-9604

; Sequence 9604, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 9604

; LENGTH: 2799

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-9604

Query Match 1.6%; Score 43.8; DB 4; Length 2799;

Best Local Similarity 47.5%; Pred. No. 0.027;

Matches 162; Conservative 0; Mismatches 177; Indels 2; Gaps 1;

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Qy      2372 TTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATG 2431
          |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      1285 TTGGCACAGCTCGGCCTGTTCCGCCTGCTCGCCACGCTGCTGCC--GCCGGACGTACCAG 1342

Qy      2432 CAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCG 2491
          |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      1343 CCGGCGGCCTGTTCCCCGCCTTCGCCGGGGTGCACCAGGCCTGGTATCGCTGGCCGGCT 1402

Qy      2492 GCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGT 2551
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      1403 TCGCCCTCCCGCCGCTGGCAGCCCTGGGCCGGGTACCGCCGTTGCGGGTCTGCGCAGCG 1462

Qy      2552 CGGCCGGGCACACTGGCCTTCTCCGTCAACCCTCTTACCATCTTTGCATTTGTCTGCATCA 2611
          |  |||  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      1463 ACCTGCTGCCGGTGCCGATGCGCACCTGGATGGCCTACGCCTGCGCCCTGCTCGCCCTGG 1522

Qy      2612 GCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCT 2671
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      1523 GCCTGATCATGTGGCGGTTGAGTCTCGACCTGAAGCTGACCCTCGCCCTGCTCGGCGGCG 1582

Qy      2672 GCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTC 2712
          ||  |  |||||  |||  |  |||  |||
Db      1583 GCCTGGTCGCCACGCTGGTGCTCGGCGCCCTCCTGCTGCTC 1623
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RESULT 13

US-09-103-840A-1/c

```
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
```

```
Query Match          1.6%; Score 43.4; DB 3; Length 4411529;
Best Local Similarity 47.3%; Pred. No. 5.2;
Matches 131; Conservative 0; Mismatches 146; Indels 0; Gaps 0;
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```
Qy      2241 CGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGG 2300
        |||  |||  ||  |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      3932453 CGGCCCCGCCGGCCCCGCCGGCGCGCGGCGTTACCGCCAGTCCCACCCGCGCCGCGTCCG
3932394
```

```
Qy      2301 GGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTTCAGTCACAGCTGTTGT 2360
        ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      3932393 CGCCAATCCGCTGGCATTATCAGCACCGGAGCCACCCATGCCGCCGGCGCCGCTTGGC
3932334
```

```
Qy      2361 TTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCA 2420
        ||  ||  |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      3932333 CGCCGGTGCCGCCGGCACCGGAGCCGTTGATGCCGCCGGCAATGGCGTTGCCGCCCT
3932274
```

```
Qy      2421 GGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTT 2480
        ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      3932273 GGCCGCCGACGCCGCCGGCCCCGCCAGCGAACCCGGTACCACCGGTTAGACCTGTGCTGG
3932214
```

```
Qy      2481 CCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATC 2517
        |  |||  ||||  ||  ||  |||  |||||  |
Db      3932213 CGGGGGCGTCGGCGCCGGCCGCTCCGGCACCGCCAGC 3932177
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RESULT 14
US-09-252-991A-5866
; Sequence 5866, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5866
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5866

Query Match 1.5%; Score 42.2; DB 4; Length 660;
Best Local Similarity 46.7%; Pred. No. 0.03;
Matches 134; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

```

Qy      2434 GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGC 2493
          | | | | | | | | | | | | | | | | | | | | | | |
Db      302 GTCGTCGCCCTGGTCATGCTGGTCCGCGGCTTCGCCGACGCGATCATGATGCGCGGCCAA 361

Qy      2494 CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCG 2553
          | | | | | | | | | | | | | | | | | | | | | |
Db      362 CTGGCCCTGGCCGAAGGCGCCAACCACGGCTACCTGCCGCCGGAGCACTACGACCAGATC 421

Qy      2554 GCCGGCACACTGGCCTTCTCCGTCAACCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
          | | | | | | | | | | | | | | | | | | | | | |
Db      422 TTCACGCGCATGGCGTGATCATGATCATCTTCATGGCCATGCCGTTTCATGACCGGCCTG 481

Qy      2614 GTGCTCTTGTAACGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGC 2673
          | | | | | | | | | | | | | | | | | | | | | |
Db      482 ATGAACCTGGCCGTGCCGCTGCAGATCGGCGCGCGCGACGTGGCGTTCCCTTCCTCAAC 541

Qy      2674 AAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACAT 2720
          | | | | | | | | | | | | | | | | | | | | | |
Db      542 TCGCTGAGCTTCTGGCTGCTCGTGGTCAGCGCCATGCTGGTCAACGT 588

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RESULT 15

US-09-252-991A-5825
; Sequence 5825, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5825
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5825

Query Match 1.5%; Score 42.2; DB 4; Length 1983;
Best Local Similarity 46.7%; Pred. No. 0.063;
Matches 134; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

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Qy      2434 GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCTGGGCATCGGC 2493
          | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      193  GTCGTCGCCCTGGTCATGCTGGTCCGCGGCTTCGCCGACGCGATCATGATGCGCGGCCAA 252

Qy      2494 CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCG 2553
          | | | | | | | | | | | | | | | | | | | | | | | | |
Db      253  CTGGCCCTGGCCGAAGGCGCCAACCACGGCTACCTGCCGCCGGAGCACTACGACCAGATC 312

Qy      2554 GCCGGCACACTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
          | | | | | | | | | | | | | | | | | | | | | | | |
Db      313  TTCACCGCGCATGGCGTGATCATGATCATCTTCATGGCCATGCCGTTTCATGACCGGCCTG 372

Qy      2614 GTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGC 2673
          | | | | | | | | | | | | | | | | | | | | | | |
Db      373  ATGAACCTGGCCGTGCCGCTGCAGATCGGCGCGCGACGTGGCGTTCCCCTTCCTCAAC 432

Qy      2674 AAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACAT 2720
          | | | | | | | | | | | | | | | | | | | | | | |
Db      433  TCGCTGAGCTTCTGGCTGCTCGTGGTCAGCGCCATGCTGGTCAACGT 479
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Search completed: June 25, 2004, 15:37:21
Job time : 228.931 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 07:13:27 ; Search time 1117.99 Seconds
(without alignments)
11333.972 Million cell updates/sec

Title: US-10-054-680-1
Perfect score: 2766
Sequence: 1 atggcgtgggttaaggttgca.....gctacatcaaggggttctaa 2766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match	Length	DB	ID	Description
1	2766	100.0	2766	14	US-10-054-680-1	Sequence 1, Appli
2	2766	100.0	3812	14	US-10-054-680-5	Sequence 5, Appli
3	2761.2	99.8	2782	9	US-09-804-474A-1	Sequence 1, Appli
4	2733.4	98.8	2781	15	US-10-275-116-1	Sequence 1, Appli
5	2673.2	96.6	2685	15	US-10-114-153-5	Sequence 5, Appli
6	2657.6	96.1	2840	15	US-10-114-153-3	Sequence 3, Appli
7	2367.2	85.6	2813	15	US-10-114-153-1	Sequence 1, Appli
8	1786.4	64.6	2534	15	US-10-256-537-1	Sequence 1, Appli
9	1786.4	64.6	2534	15	US-10-256-537-3	Sequence 3, Appli
10	1784.8	64.5	126512	9	US-09-804-474A-3	Sequence 3, Appli
11	1784.6	64.5	1863	14	US-10-054-680-3	Sequence 3, Appli
12	1277	46.2	4282	15	US-10-281-866-1	Sequence 1, Appli
13	1277	46.2	4282	15	US-10-281-866-3	Sequence 3, Appli
14	1270.8	45.9	3004	16	US-10-388-934-506	Sequence 506, App
15	1227.8	44.4	4087	9	US-09-901-419-1	Sequence 1, Appli
16	1207.2	43.6	6106	16	US-10-062-674-1648	Sequence 1648, Ap
17	897.4	32.4	1187	13	US-10-243-552-809	Sequence 809, App
18	821.4	29.7	823	15	US-10-029-386-20265	Sequence 20265, A
19	787.2	28.5	1836	9	US-09-864-761-16939	Sequence 16939, A
20	503.4	18.2	505	15	US-10-029-386-6536	Sequence 6536, Ap
21	494	17.9	551	15	US-10-029-386-4103	Sequence 4103, Ap
22	366	13.2	366	15	US-10-029-386-17804	Sequence 17804, A
23	336.4	12.2	507	15	US-10-029-386-4003	Sequence 4003, Ap
c 24	219.4	7.9	381	9	US-09-864-761-1172	Sequence 1172, Ap
25	210.2	7.6	502	15	US-10-029-386-7461	Sequence 7461, Ap
26	208.4	7.5	280	15	US-10-029-386-21161	Sequence 21161, A
27	186.4	6.7	491	9	US-09-864-761-646	Sequence 646, App
28	186.2	6.7	276	9	US-09-864-761-17437	Sequence 17437, A
29	180	6.5	180	15	US-10-029-386-17706	Sequence 17706, A
30	169	6.1	477	10	US-09-918-995-2005	Sequence 2005, Ap
31	164.2	5.9	459	9	US-09-864-761-102	Sequence 102, App
32	146.6	5.3	1132	16	US-10-369-493-30006	Sequence 30006, A
33	108	3.9	1302	13	US-10-243-552-276	Sequence 276, App
c 34	95	3.4	151	9	US-09-864-761-17938	Sequence 17938, A
35	91.4	3.3	1792	16	US-10-369-493-29835	Sequence 29835, A
36	76.6	2.8	1617	9	US-09-938-842A-2591	Sequence 2591, Ap
37	76.6	2.8	1617	11	US-09-938-842A-2591	Sequence 2591, Ap
38	73.4	2.7	968	13	US-10-424-599-94222	Sequence 94222, A
39	60	2.2	128	9	US-09-864-761-20736	Sequence 20736, A
c 40	60	2.2	136	15	US-10-029-386-23072	Sequence 23072, A
41	60	2.2	467	9	US-09-864-761-3975	Sequence 3975, Ap
c 42	60	2.2	546	13	US-10-027-632-247268	Sequence 247268,
c 43	60	2.2	546	16	US-10-027-632-247268	Sequence 247268,
c 44	60	2.2	599	15	US-10-029-386-9372	Sequence 9372, Ap
45	60	2.2	1173	13	US-10-027-632-100718	Sequence 100718,

ALIGNMENTS

RESULT 1

US-10-054-680-1

; Sequence 1, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

```
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and
Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2766
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-680-1
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Query Match          100.0%; Score 2766; DB 14; Length 2766;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy    241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy    361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy    421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC 480

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
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Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380

Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATT CAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATT CAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAA ACTA	1980
Db	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAA ACTA	1980
Qy	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Db	1981	GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC	2100
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280

Db	2221		CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Qy	2281		ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Db	2281		ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA	2340
Qy	2341		GATTTCAGTCACAGCTGTTGTTTTCTGTTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2341		GATTTCAGTCACAGCTGTTGTTTTCTGTTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Qy	2401		AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Db	2401		AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460
Qy	2461		AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Db	2461		AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC	2520
Qy	2521		TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Db	2521		TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC	2580
Qy	2581		CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Db	2581		CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC	2640
Qy	2641		CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Db	2641		CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG	2700
Qy	2701		AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Db	2701		AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG	2760
Qy	2761		TTCTAA 2766	
Db	2761		TTCTAA 2766	

RESULT 2

US-10-054-680-5

; Sequence 5, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0301-USA

; CURRENT APPLICATION NUMBER: US/10/054,680

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,384

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5
; LENGTH: 3812
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-680-5

Query Match 100.0%; Score 2766; DB 14; Length 3812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	618	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	677
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	678	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	737
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	738	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	797
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	798	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	857
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	858	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	917
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	918	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	977
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	978	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	1037
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	1038	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	1097
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1098	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1157
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1158	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1217
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1218	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1277
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1278	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1337

Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1338	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1397
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1398	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1457
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1458	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1517
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1518	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1577
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1578	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1637
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1638	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1697
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1698	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1757
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1758	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1817
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1818	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1877
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1878	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1937
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1938	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1997
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1998	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2057
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2058	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2117
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	2118	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	2177

Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	2178	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	2237
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	2238	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	2297
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2298	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2357
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	2358	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	2417
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	2418	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	2477
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	1920
Db	2478	CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA	2537
Qy	1921	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	1980
Db	2538	GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA	2597
Qy	1981	GAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2040
Db	2598	GAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTGGACAACTGATCAAGAAG	2657
Qy	2041	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC	2100
Db	2658	ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATC	2717
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2160
Db	2718	ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC	2777
Qy	2161	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2220
Db	2778	TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG	2837
Qy	2221	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2280
Db	2838	CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC	2897
Qy	2281	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAA	2340
Db	2898	ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTTGGTCTCAA	2957
Qy	2341	GATTCACTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	2400
Db	2958	GATTCACTCACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCAGATACGTTTGCC	3017
Qy	2401	AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC	2460

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Db      3018 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 3077

Qy      2461 AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3078 AGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 3137

Qy      2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3138 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 3197

Qy      2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3198 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 3257

Qy      2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3258 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 3317

Qy      2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3318 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 3377

Qy      2761 TTCTAA 2766
      |||||
Db      3378 TTCTAA 3383

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RESULT 3

US-09-804-474A-1

; Sequence 1, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000891

; CURRENT APPLICATION NUMBER: US/09/804,474A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2782

; TYPE: DNA

; ORGANISM: Human

US-09-804-474A-1

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Query Match          99.8%; Score 2761.2; DB 9; Length 2782;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69

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Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	70	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	130	ACAGGGCAGAACAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	249
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	250	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	369
Qy	361	ACCAGCACAACTACTATTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	370	ACCAGCACAACTACTATTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	429
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	430	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	669
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	670	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	729
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	730	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	909
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960

Db	910	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC	969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1030	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1450	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1510	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1570	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1629
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1630	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1689
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1690	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1749
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT	1800

Db 1750 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTGAAAACCATAAGGGTT 1809

Qy 1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
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Db 1810 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1869

Qy 1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
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Db 1870 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1929

Qy 1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA 1980
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Db 1930 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAATA 1989

Qy 1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
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Db 1990 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2049

Qy 2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC 2100
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Db 2050 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACAGTTCATGGAGGCCATC 2109

Qy 2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
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Db 2110 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2169

Qy 2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
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Db 2170 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2229

Qy 2221 CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
 |||

Db 2230 CCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2289

Qy 2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA 2340
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Db 2290 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAA 2349

Qy 2341 GATTTCAGTCACAGCTGTTGTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC 2400
 |||

Db 2350 GATTTCAGTCACAGCTGTTGTTTTCGTGGCATTGTCACCTCTGTCCCAGATACGTTTGCC 2409

Qy 2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
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Db 2410 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2469

Qy 2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
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Db 2470 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2529

Qy 2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTGGCCGGGCACACTGGCCTTCTCCGTACAC 2580
 |||

Db 2530 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTGGCCGGGCACACTGGCCTTCTCCGTACAC 2589

Qy 2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
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Db 2590 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2649

Qy 2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
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 Db 2650 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2709
 Qy 2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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 Db 2710 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2769
 Qy 2761 TTCTAA 2766
 |||
 Db 2770 TTCTAA 2775



RESULT 4

US-10-275-116-1

; Sequence 1, Application US/10275116
 ; Publication No. US20030096312A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Merck Patent GmbH
 ; TITLE OF INVENTION: No. US20030096312A1el natrium-calium exchanger protein
 ; FILE REFERENCE: HNCX3CWWS
 ; CURRENT APPLICATION NUMBER: US/10/275,116
 ; CURRENT FILING DATE: 2002-11-01
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2781
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(2781)

4/30/01

US-10-275-116-1

Query Match 98.8%; Score 2733.4; DB 15; Length 2781;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 2762; Conservative 0; Mismatches 1; Indels 18; Gaps 1;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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 Db 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
 Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
 |||
 Db 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
 Qy 121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 180
 |||
 Db 121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 180
 Qy 181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
 |||
 Db 181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
 Qy 241 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACCACTATTCTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140

Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAAACCATAAGGGTT	1800
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Qy	1861	CCGAAATGGATGGAACGTGGAATATC-----AGATGTGACAGACAGG	1902
Db	1861	CCGAAATGGATGGAACGTGGAATATCAGGTGTGAGATTCTTTAAAGATGTGACAGACAGG	1920
Qy	1903	AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG	1962
Db	1921	AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG	1980

Qy	1963	GGTGAACACCCCAAAGTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG	2022
Db	1981	GGTGAACACCCCAAAGTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG	2040
Qy	2023	GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGAC	2082
Db	2041	GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGAC	2100
Qy	2083	CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG	2142
Db	2101	CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG	2160
Qy	2143	GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG	2202
Db	2161	GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG	2220
Qy	2203	GTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC	2262
Db	2221	GTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC	2280
Qy	2263	TCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGC	2322
Db	2281	TCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGC	2340
Qy	2323	TGCACCATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTCGTGGCATTGGGCACCTCT	2382
Db	2341	TGCACCATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTCGTGGCATTGGGCACCTCT	2400
Qy	2383	GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC	2442
Db	2401	GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC	2460
Qy	2443	ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGG	2502
Db	2461	ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGG	2520
Qy	2503	TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACA	2562
Db	2521	TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTGCGCCGGCACA	2580
Qy	2563	CTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG	2622
Db	2581	CTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG	2640
Qy	2623	TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC	2682
Db	2641	TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC	2700
Qy	2683	ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC	2742
Db	2701	ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC	2760
Qy	2743	TATTGCTACATCAAGGGGTTT	2763
Db	2761	TATTGCTACATCAAGGGGTTT	2781

✓ RESULT 5

US-10-114-153-5

; Sequence 5, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennnda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Tchernev, Velizar

; APPLICANT: Gangolli, Esha

; APPLICANT: Vernet, Corine

; APPLICANT: Spytek, Kimberly

; APPLICANT: Malyankar, Uriel

; APPLICANT: Patturajan, Meera

; APPLICANT: Miller, Charles

; APPLICANT: Taupier, Raymond J. Jr.

; APPLICANT: Heyes, Melvyn

; APPLICANT: Ju, Jingfang

; APPLICANT: Peyman, John

; APPLICANT: Catterton, Elina

; APPLICANT: MacDougall, John

; APPLICANT: Edinger, Shlomit

; APPLICANT: Stone, David

; APPLICANT: Mazur, Ann

; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS

; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE

; FILE REFERENCE: 21402-322A

; CURRENT APPLICATION NUMBER: US/10/114,153

; CURRENT FILING DATE: 2002-08-06

; PRIOR APPLICATION NUMBER: 60/281086

; PRIOR FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 60/281906

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282020

; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/282930

; PRIOR FILING DATE: 2001-04-10

; PRIOR APPLICATION NUMBER: 60/283512

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: 60/283444

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: 60/283657

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283710

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283678

; PRIOR FILING DATE: 2001-04-13

4/1/01

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; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 5
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2685)
US-10-114-153-5
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Query Match          96.6%; Score 2673.2; DB 15; Length 2685;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2675; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      86 GAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 145
      || | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2  GATCCGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 61

Qy     146 CAGGGTCATCGGACTGCAAGGAGGGTGTCTCCTGCCAATCTGGTACCCGGAGAACCCTT 205
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 CAGGGTCATCGGACTGCAAGGAGGGTGTCTCCTGCCAATCTGGTACCCGGAGAACCCTT 121

Qy     206 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 265
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 181

Qy     266 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 325
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 241

Qy     326 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCT 385
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCT 301

Qy     386 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTTCCTCTGCTCCTGAGATAC 445
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTTCCTCTGCTCCTGAGATAC 361

Qy     446 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTA 505
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTA 421

Qy     506 CCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGA 565
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     422 CCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGA 481

Qy     566 TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTT 625
      |||||||||||||||||||||||| |||||||||||||||||||||||||
Db     482 TCCCAGACGGAGAGACTCGCAAGATCAACATCTACGAGTCTTCTTCATCACCGCTGCTT 541

Qy     626 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 685
      |||||||||||||||||||||||| |||||||||||||||||||||||||
Db     542 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 601
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Qy	686	TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCT	745
Db	602	TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCT	661
Qy	746	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	805
Db	662	GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA	721
Qy	806	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	865
Db	722	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	781
Qy	866	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAGGAAG	925
Db	782	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAGGAAG	841
Qy	926	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	985
Db	842	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	901
Qy	986	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA	1045
Db	902	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA	961
Qy	1046	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1105
Db	962	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1021
Qy	1106	TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1165
Db	1022	TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1081
Qy	1166	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1225
Db	1082	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1141
Qy	1226	AGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA	1285
Db	1142	AGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA	1201
Qy	1286	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1345
Db	1202	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1261
Qy	1346	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1405
Db	1262	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1321
Qy	1406	TTGATGACGACATTTTGGAGGAGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1465
Db	1322	TTGATGACGACATTTTGGAGGAGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1381
Qy	1466	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1525
Db	1382	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1441
Qy	1526	CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1585

Db	1442	CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1501
Qy	1586	CAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGTGTTATGG	1645
Db	1502	CAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGTGTTATGG	1561
Qy	1646	AGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGTACAGTCATCGTCCCCTTTAGGACAG	1705
Db	1562	AGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGTACAGTCATCGTCCCCTTTAGGACAG	1621
Qy	1706	TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1765
Db	1622	TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1681
Qy	1766	TCAAGAATGATGAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACG	1825
Db	1682	TCAAGAATGATGAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACG	1741
Qy	1826	AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT	1885
Db	1742	AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT	1801
Qy	1886	CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1945
Db	1802	CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1861
Qy	1946	TGGGAAAGCCAGTATTGGGTGAACACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATG	2005
Db	1862	TGGGAAAGCCAGTATTGGGTGAACACCCCAAACCTAGAAGTCATCATTGAAGAGTCCTATG	1921
Qy	2006	AGTTCAAGACTACGGTGGACAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA	2065
Db	1922	AGTTCAAGACTACGGTGGACAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA	1981
Qy	2066	CCCATTCTGGAGGGACCAAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGG	2125
Db	1982	CCCATTCTGGAGGGACCAAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGG	2041
Qy	2126	ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC	2185
Db	2042	ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC	2101
Qy	2186	TGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCT	2245
Db	2102	TGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCT	2161
Qy	2246	GGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACC	2305
Db	2162	GGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACC	2221
Qy	2306	TGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTAGTACAGCTGTTGTTTTTCG	2365
Db	2222	TGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTAGTACAGCTGTTGTTTTTCG	2281
Qy	2366	TGGCATTGTCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATG	2425

Db 2282 TGGCATTGTCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATG 2341

Qy 2426 TATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGG 2485
 |||

Db 2342 TATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGG 2401

Qy 2486 GCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCC 2545
 |||

Db 2402 GCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCC 2461

Qy 2546 ACGTGTGGCCGGCAGCACTGGCCTTCTCCGTCAACCCTCTTCACCATCTTTGCATTTGTCT 2605
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Db 2462 ACGTGTGGCCGGCAGCACTGGCCTTCTCCGTCAACCCTCTTCACCATCTTTGCATTTGTCT 2521

Qy 2606 GCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCC 2665
 |||

Db 2522 GCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCC 2581

Qy 2666 GTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCT 2725
 |||

Db 2582 GTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCT 2641

Qy 2726 TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTT 2763
 |||

Db 2642 TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTT 2679

✓ RESULT 6

US-10-114-153-3

; Sequence 3, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara

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; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 3
; LENGTH: 2840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(2838)
US-10-114-153-3

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Query Match          96.1%; Score 2657.6; DB 15; Length 2840;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2712; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 60
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Db      63 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 122

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      123 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 182

Qy      121 ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      183 ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 242

Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

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Db	243	 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	302
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	303	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	362
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	363	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	422
Qy	361	ACCAGCACAACCACTATTCCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	423	ACCAGCACAACCACTATTCCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	482
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	483	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	542
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	543	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	602
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	603	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	662
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTCCTACATCTGGCTCTATATGATT	660
Db	663	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTCCTACATCTGGCTCTATATGATT	722
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	723	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	782
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	783	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	842
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	843	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	902
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	903	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	962
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	963	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1022
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1023	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1082
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080

Db 1083 TACTATGCTCTTTCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1142
 Qy 1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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 Db 1143 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1202
 Qy 1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1203 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1262
 Qy 1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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 Db 1263 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1322
 Qy 1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1323 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1382
 Qy 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1383 AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1442
 Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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 Db 1443 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1502
 Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1503 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1562
 Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1563 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1622
 Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
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 Db 1623 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1682
 Qy 1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT 1680
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 Db 1683 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT 1742
 Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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 Db 1743 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1802
 Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACATAAGGGTT 1800
 ||||||||||||||||||||||||||||||||||||||||||||| ||||| |
 Db 1803 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTCAAAACAATTACATC 1862
 Qy 1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
 || || | |||| |||| || | | | ||||| ||||| | |
 Db 1863 AAGGTAATTGATGATGAGGCATATGAGAAAAACAAGAATTACTTCATTGAGATGATGGGC 1922
 Qy 1861 CCGAAATGGATGGAACGTGGAATATCAGATGTG-----ACAGACAGGAAGCTG 1908
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 Db 1923 CCCCAGCATGGTGGATATGAGTTTTTCAGAAAGCGCTCCTGTTATCTCCAGACAGGAAGCTG 1982

Qy	1909	ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA	1968
Db	1983	ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA	2042
Qy	1969	CACCCCAAACCTAGAAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAA	2028
Db	2043	CACCCCAAACCTAGAAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAA	2102
Qy	2029	CTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTC	2088
Db	2103	CTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAAGTTC	2162
Qy	2089	ATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAG	2148
Db	2163	ATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAG	2222
Qy	2149	AGGCTGCCCTCCTGCTTTGACTACGTGCAGTGCAGTTCCTGACTGTCTTCTGGAAGGTGCTG	2208
Db	2223	AGGCTGCCCTCCTGCTTTGACTACGTGCAGTGCAGTTCCTGACTGTCTTCTGGAAGGTGCTG	2282
Qy	2209	TTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATC	2268
Db	2283	TTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATC	2342
Qy	2269	CTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACC	2328
Db	2343	CTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACC	2402
Qy	2329	ATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCA	2388
Db	2403	ATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTTCGTGGCATTGGGCACCTCTGTCCCA	2462
Qy	2389	GATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGC	2448
Db	2463	GATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGC	2522
Qy	2449	AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG	2508
Db	2523	AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG	2582
Qy	2509	GCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCACGTGTGCGCCGGCACACTGGCC	2568
Db	2583	GCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCACGTGTGCGCCGGCACACTGGCC	2642
Qy	2569	TTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGA	2628
Db	2643	TTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGA	2702
Qy	2629	AGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACA	2688
Db	2703	AGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACA	2762
Qy	2689	TGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGC	2748
Db	2763	TGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGC	2822


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; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 1
; LENGTH: 2813
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(2793)
US-10-114-153-1
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Query Match          85.6%; Score 2367.2; DB 15; Length 2813;
Best Local Similarity 91.2%; Pred. No. 0;
Matches 2542; Conservative 0; Mismatches 223; Indels 21; Gaps 2;
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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db      9 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 68

Qy     61 TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 128

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 188

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 248

Qy    241 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 308

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 368

Qy    361 ACCAGCACAACCCTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 ACCAGCACAACCCTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC 428

Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 488

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 ATTGCTGGTGATCTGGGACCTTCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 548
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Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	549	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	608
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	609	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	668
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	669	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	728
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	729	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	788
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	789	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	848
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Db	849	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	908
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	909	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	968
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	969	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1028
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1029	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1088
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
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Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1149	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1208
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1209	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1268
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1269	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1328
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1329	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1388

Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1389	CAGAAGGAGTTCTCCGTGGGCATAAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1448
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1449	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1508
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1509	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1568
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATT CAT	1620
Db	1569	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATT CAT	1628
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1629	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1688
Qy	1681	ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1689	ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1748
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTGAAAACCAT AAGGGTT	1800
Db	1749	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTGAAAACCTTTCAGGTG	1808
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA	1860
Db	1809		1868
Qy	1861	CCGAAATGGATGGAACGTGGAATATCAGATGTGACA-----GACAGG	1902
Db	1869		1928
Qy	1903	AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG	1962
Db	1929		1988
Qy	1963	GGTGAACACCCCCAAACTAGAAGTCATCATTGAAGAGTCCATGAGTTCAAGACTACGGTG	2022
Db	1989		2048
Qy	2023	GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGAC	2082
Db	2049		2108
Qy	2083	CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAA---TCC	2139
Db	2109		2168
Qy	2140	GGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGG	2199
Db	2169		2228
Qy	2200	AAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCC	2259

; TYPE: DNA
; ORGANISM: Homo sapien
US-10-256-537-1

Query Match 64.6%; Score 1786.4; DB 15; Length 2534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db     343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
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Db    463 ACAGGGCAGAACAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 522

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db    523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy    241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db    583 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy    361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db    703 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy    421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480
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Db    763 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 822

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 882

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db    883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db    943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db	1063	 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1122
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1123	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1182
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1183	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1242
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1243	 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1302
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1303	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1362
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1363	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1422
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1423	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1482
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1483	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1542
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1543	 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1602
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1603	 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1662
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1663	 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1722
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1723	 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1782
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1783	 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1842
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1843	 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1902
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620

Db 1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962

Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
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Db 1963 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 2022

Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db 2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGTGAAA 1788
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Db 2083 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGTGTAA 2130

RESULT 9

US-10-256-537-3

; Sequence 3, Application US/10256537
 ; Publication No. US20030162196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carroll, Joseph M.
 ; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
 ; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER
 ; FILE REFERENCE: MPI01-231P1RM
 ; CURRENT APPLICATION NUMBER: US/10/256,537
 ; CURRENT FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/325,737
 ; PRIOR FILING DATE: 2001-09-28
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 2534
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (343)...(2130)
 US-10-256-537-3

Query Match 64.6%; Score 1786.4; DB 15; Length 2534;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db 343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy 61 TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db 403 TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy 121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
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Db 463 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 522

Qy 181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db	523	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	582
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
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Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	643	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	702
Qy	361	ACCAGCACAAACCACTATTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	703	ACCAGCACAAACCACTATTGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	762
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	763	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	822
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	823	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	882
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTGCCTACATCTGGCTCTATATGATT	660
Db	943	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTGCCTACATCTGGCTCTATATGATT	1002
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
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Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1063	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1122
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1123	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1182
Qy	841	CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1183	CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1242
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1243	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1302
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1303	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1362
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1363	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1422

Qy 1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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 Db 1423 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482
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 Db 1483 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542
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 Db 1543 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602
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 Db 1603 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1662
 Qy 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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 Db 1663 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722
 Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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 Db 1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782
 Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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 Db 1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842
 Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
 |||
 Db 1843 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1902
 Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
 |||
 Db 1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1962
 Qy 1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
 |||
 Db 1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2022
 Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 |||
 Db 2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082
 Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAA 1788
 |||
 Db 2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGTAA 2130

RESULT 10

US-09-804-474A-3

; Sequence 3, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
 PROTEINS,
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CL000891
 ; CURRENT APPLICATION NUMBER: US/09/804,474A
 ; CURRENT FILING DATE: 2001-03-13
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 126512
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(126512)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-804-474A-3

Query Match 64.5%; Score 1784.8; DB 9; Length 126512;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1786; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	2010	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	2069
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	2070	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	2129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	2130	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	2189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	2190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	2249
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	2250	TTTGTGGCCCTGATATACATGTTCCCTTGGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	2309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	2310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	2369
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	2370	ACCAGCACAACAACCTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	2429
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	2430	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	2489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	2490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	2549

Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	2550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	2609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	2610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	2669
Qy	661	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	2670	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	2729
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	2730	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	2789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	2790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	2849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	900
Db	2850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAAC	2909
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	2910	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	2969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	2970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	3029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	3030	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	3089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	3090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	3149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	3150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	3209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	3210	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	3269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	3270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	3329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	3330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	3389

Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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 Db 3390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 3449

Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
 |||
 Db 3450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 3509

Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
 |||
 Db 3510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 3569

Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
 |||
 Db 3570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 3629

Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
 |||
 Db 3630 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 3689

Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 |||
 Db 3690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 3749

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGAAA 1788
 |||
 Db 3750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGTAA 3797

RESULT 11

US-10-054-680-3

; Sequence 3, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. US20020132998A1 Human Ion Exchanger Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0301-USA

; CURRENT APPLICATION NUMBER: US/10/054,680

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,384

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 1863

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-054-680-3

Query Match 64.5%; Score 1784.6; DB 14; Length 1863;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 60

Db	1		1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61		TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61		TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121		ACAGGGCAGAACAATGAGTCCTGTT CAGGGTCATCGGACTGCAAGGAGGGTGT CATCCTG	180
Db	121		ACAGGGCAGAACAATGAGTCCTGTT CAGGGTCATCGGACTGCAAGGAGGGTGT CATCCTG	180
Qy	181		CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181		CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241		TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241		TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301		TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301		TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361		ACCAGCACAAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361		ACCAGCACAAACCACTATTCCGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421		CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421		CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481		ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481		ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541		ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541		ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601		CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601		CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661		CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661		CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721		TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721		TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841		CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900

Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740

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Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC---TGTGAAAACCATAAG 1796
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Db      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800

Qy      1797 GGTТААAАTAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
```

Db 508 TCCGCACCTGAGATCCTGCTGTCTAGTCATCGAAGTCTGCGGCCACAACCTCCAGGCGGGT 567
 Qy 490 GATCTGGGACCTTCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGC 549
 || ||||| || ||||| || || || || ||||| ||||| || ||||| ||
 Db 568 GAGCTGGGCCCAGGCACCATCGTGGGCAGCGCTGCCTTCAACATGTTTGTGGTCATCGCC 627
 Qy 550 ATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTC 609
 | || ||||| ||||| || ||||| ||||| ||||| || ||||| ||
 Db 628 GTGTGCATCTACGTATCCCAGCCGGCGAGAGCCGCAAGATCAAGCACCTGAGAGTCTTC 687
 Qy 610 TTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTC 669
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 Db 688 TTTGTCACTGCCTCTTGGAGCATCTTCGCCTATGTCTGGCTTTATCTCATCCTTGCTGTT 747
 Qy 670 TTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTG 729
 || ||||| ||||| ||||| ||||| || || || || || ||||| || ||||| ||
 Db 748 TTTTCCCCCGGTGTGGTCCAGGTGTGGGAGGCGCTGCTGACCCTGGTCTTCTTCCCGGTG 807
 Qy 730 TGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAA 789
 || || | | ||||| ||||| || || || ||||| ||||| || ||||| ||
 Db 808 TGCCTGGTATTTCGCCTGGATGGCCGACAAGCGGCTGCTCTTCTACAAGTACGTGTACAAG 867
 Qy 790 AAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAG 849
 ||||| || || || || || ||||| || ||||| ||||| || ||||| ||
 Db 868 CGCTACCGCACCGACCCACGCAGCGGCATCATCATAGGCGCCGAGGGCGACCCCCGAAG 927
 Qy 850 GGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAA----- 899
 |||| |||| |||| || || || || || || || || || || || || ||
 Db 928 AGCATCGAGCTGGACGGCACGTTTCGTGGGCGCCGAGGCCCCAGGTGAGCTGGGCGGCCTG 987
 Qy 900 --CCTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATT 957
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 Db 988 GGCCCGGGCCCCGCGGAGGCGCGGAGCTGGACGCCAGCCGCGCGAGGTATCCAGATC 1047
 Qy 958 CTCAAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCC 1017
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 Db 1048 CTCAAGGACCTCAAGCAGAAGCACCCGGACAAGGATCTGGAGCAGCTGGTGGGCATCGCC 1107
 Qy 1018 AATTACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACT 1077
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 Db 1108 AACTACTACGCGCTGCTGCACCAGCAGAAGAGCCGCGCCTTCTACCGCATCCAGGCCACG 1167
 Qy 1078 CGTATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAG 1137
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 Db 1168 CGGCTGATGACCGGCGCCGGGAACGTGCTGCGCAGACACGCGGCGGACGCCTCGCGCAGG 1227
 Qy 1138 GCCTCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTC 1197
 || | | ||||| || || || || || || || || || || || || || || || ||
 Db 1228 GCGGC---GCCGGCCGAGGGCGCGGGCGAGGACGAAGACGACGGCGCCAGCCGCATCTTC 1284
 Qy 1198 TTTGACCCATGTTCTTACCAGTGCCTGGGAACTGTGGGGCTGTACTCCTGACAGTGGTG 1257
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 Db 1285 TTCGAGCCTAGCCTCTACCACTGCCTGGGAACTGCGGCTCCGTGCTGCTGTCCGTACG 1344
 Qy 1258 AGGAAAGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCT 1317
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 Db 1345 TGCCAGGGCGGCGAGGGCAACAGCACCTTCTACGTGGACTACCGCACTGAGGACGGCTCT 1404

Qy	1318	GCCAAATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAG	1377
Db	1405	GCCAAGGCGGGCTCCGACTACGAGTACAGCGAGGGCACGCTGGTGTTCAAACCAGGCGAG	1464
Qy	1378	ACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACAC	1437
Db	1465	ACGCAGAAGGAGCTGCGCATCGGCATCATCGACGACGACATCTTCGAGGAGGACGAGCAT	1524
Qy	1438	TTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCT	1497
Db	1525	TTCTTCGTGCGGCTGCTGAACCTGCGCGTGGGCGACGCGCAGGGCATGTTTCGAGCCG---	1581
Qy	1498	CCAGCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCC	1557
Db	1582	-----GACGGCGGCGGGCGGCCCAAGGGCGGGCTGGTGGCGCCGCTGCTGGCC	1629
Qy	1558	ACAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATT	1617
Db	1630	ACCGTCACCATCCTGGACGACGACCACGCAGGCATCTTCTCCTTCCAGGACCGCCTGCTG	1689
Qy	1618	CATGTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGG	1677
Db	1690	CACGTGAGCGAGTGCATGGGCACCGTGGACGTGCGCGTCGTGCGCAGCTCGGGCGCGCGC	1749
Qy	1678	GGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGAC	1737
Db	1750	GGCACCGTGCGCCCTTCCCTACCGCACGGTGGACGGCACGGCGCGCGGGCGGCGGCGTGCAC	1809
Qy	1738	TTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGG	1797
Db	1810	TACGAGGACGCGTGC GGAGAGCTGGAGTTTGGCGACGACGAGACCATGAAAACCTCTTCAG	1869
Qy	1798	GTTAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGT	1857
Db	1870	GTGAAGATAGTTGATGACGAGGAATATGAGAAAAAGGATAATTTCTTCATTGAGCTGGGC	1929
Qy	1858	GAACCGAAATGGATGGAACGTGGAATATCAGATGTGACA-----GAC	1899
Db	1930	CAGCCCCAGTGGCTTAAGCGAGGGATTTTCAGCTCTGCTACTCAATCAAGGGGATGGGGAC	1989
Qy	1900	AGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTA	1959
Db	1990	AGGAAGCTAACAGCCGAGGAGGAGGAGGCTCGGAGGATAGCAGAGATGGGCAAGCCAGTT	2049
Qy	1960	TTGGGTGAACACCCCAAAC TAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACG	2019
Db	2050	CTTGGGGAGAACTGCCGGCTGGAGGTCATCATCGAGGAGTCATATGATTTTAAGAACACG	2109
Qy	2020	GTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTTGGAGG	2079
Db	2110	GTGGATAAACTCATCAAGAAAACGAACTTGGCCTTGGTAAATTGGGACCCATTTCATGGAGG	2169
Qy	2080	GACCAGTTCATGGAGGCCATCACCGTCAGTGCAGC---AGGGGATGAGGATGAGGATGAA	2136
Db	2170	GAGCAGTTTTTTAGAGGCAATTACGGTGAGCGCAGGGGACGAGGAGGAGGAGGAGGACGGG	2229

Qy	2137	TCCGGGGAGGAGAGGGCTGCCCTCCTGCTTTGACTACGTCATGCACCTTCCTGACTGTCTTC	2196
Db	2230		
Qy	2197	TCCCGGGAGGAGCGGGCTGCCGTCGTGCTTTGACTACGTGATGCACCTTCCTGACGGTGTTC	2289
Qy	2197	TGGAAGGTGCTGTTTGCCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTC	2256
Db	2290		
Qy	2290	TGGAAGGTGCTCTTCGCCTGTGTGCCCCCACCGAGTACTGCCACGGCTGGGCCTGCTTT	2349
Qy	2257	GCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCAC	2316
Db	2350		
Qy	2350	GGTGTCTCCATCCTGGTCATCGGCCCTGCTCACCGCCCTCATTGGGGACCTCGCCTCCAC	2409
Qy	2317	TTCGGCTGCACCATTTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTCGTGGCATTG	2376
Db	2410		
Qy	2410	TTCGGCTGCACCGTTGGCCTCAAGGACTCTGTCAATGCTGTTGTCTTCGTTGCCCTGGGC	2469
Qy	2377	ACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGAC	2436
Db	2470		
Qy	2470	ACCTCCATCCCTGACACGTTGCCAGCAAGGTGGCGGCGCTGCAGGACAGTGCGCCGAC	2529
Qy	2437	GCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCCTGGGCATCGGCCTG	2496
Db	2530		
Qy	2530	GCGTCCATCGGCAACGTGACCGGCTCCAACGCGGTGAACGTGTTCCCTTGGCCTGGGCGTC	2589
Qy	2497	GCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTCCACGTGTCGGCC	2556
Db	2590		
Qy	2590	GCCTGGTCTGTGGCCGCCGTGTACTGGGCGGTGCAGGGCCGCCCTTCGAGGTGCGCACT	2649
Qy	2557	GGCACACTGGCCTTCTCCGTACCCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTG	2616
Db	2650		
Qy	2650	GGCACGCTGGCCTTCTCCGTACGCTCTTCACCCTCTTCGCCTTCGTGGGCATTGCCGTG	2709
Qy	2617	CTCTTGTAACGAAGGCGGCCGACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAG	2676
Db	2710		
Qy	2710	CTGCTGTACCGGCGCCGCGGCACATCGGCGGCGAGCTGGGCGGCCGCGCGGACCCAAG	2769
Qy	2677	CTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTGCCACACTA	2736
Db	2770		
Qy	2770	CTCGCCACCACGCGCTCTTCCTGGGCTCTGGCTCCTGTACATCCTCTTCGCCAGCCTG	2829
Qy	2737	GAGGCCTATTGCTACATCAAGGGTTCTA	2765
Db	2830		
Qy	2830	GAGGCGTACTGCCACATCCGGGGCTTCTA	2858

; PRIOR APPLICATION NUMBER: 60/335,078

```
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4282
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (94)...(2859)
US-10-281-866-3
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Query Match          46.2%; Score 1277; DB 15; Length 4282;
Best Local Similarity 69.1%; Pred. No. 0;
Matches 1843; Conservative 0; Mismatches 775; Indels 51; Gaps 5;
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Qy      130 AACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTGCCAATCTGG 189
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      208 AGCACAGGGGGCTGCCAGGGGTCTACCGCTGCCAGCCGGGGGTGCTGCTGCCCGTGTGG 267

Qy      190 TACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCC 249
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      268 GAGCCCGACGACCCGTCGCTGGGTGACAAGGCGGCACGGGCAGTGGTGTACTTTGTGGCC 327

Qy      250 CTGATATACATGTTTCCTTGGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAA 309
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      328 ATGGTCTACATGTTTCTGGGAGTGTCCATCATCGCCGACCGTTTCATGGCGGCCATCGAG 387

Qy      310 GTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACA 369
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      388 GTCATCACGTCAAAGAGAAGGAGATCACCATCACCAAGGCCAACGGTGAGACCAGCGTG 447

Qy      370 ACCACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTC 429
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      448 GGCACCGTTCGCATCTGGAATGAGACGGTGTCCAACCTCACGCTCATGGCCCTGGGCTCC 507

Qy      430 TCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTATTGCTGGT 489
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      508 TCCGCACCTGAGATCCTGCTGTGAGTCATCGAAGTCTGCGGCCACAACCTCCAGGCGGGT 567

Qy      490 GATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGC 549
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      568 GAGCTGGGCCCAGGCACCATCGTGGGCAGCGCTGCCTTCAACATGTTTGTGGTCATCGCC 627

Qy      550 ATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTC 609
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      628 GTGTGCATCTACGTGATCCCAGCCGGCGAGAGCCGCAAGATCAAGCACCTGAGAGTCTTC 687

Qy      610 TTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTC 669
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      688 TTTGTCACTGCCTCTTGGAGCATCTTCGCCTATGTCTGGCTTTATCTCATCCTTGCTGTT 747

Qy      670 TTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTTCCAGTG 729
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      748 TTTTCCCCCGGTGTGGTCCAGGTGTGGGAGGCGCTGCTGACCCTGGTCTTCTTCCCGGTG 807

Qy      730 TGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAA 789
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Db	808	TGCGTGGTATTTCGCCTGGATGGCCGACAAGCGGCTGCTCTTCTACAAGTACGTGTACAAG	867
Qy	790	AAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAG	849
Db	868	CGCTACCGCACCGACCCACGCAGCGGCATCATCATAGGCGCCGAGGGCGACCCCCGAAG	927
Qy	850	GGCATTGAGATGGATGGGAAAATGATGAATCCCATTTTCTAGATGGGAA-----	899
Db	928	AGCATCGAGCTGGACGGCACGTTCTGTGGGCGCCGAGGCCCCAGGTGAGCTGGGCGGCCTG	987
Qy	900	--CCTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATT	957
Db	988	GGCCCGGGCCCCGCCGAGGCGCGGAGCTGGACGCCAGCCGCCGCGAGGTCATCCAGATC	1047
Qy	958	CTCAAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCC	1017
Db	1048	CTCAAGGACCTCAAGCAGAAGCACCCGACAAGGATCTGGAGCAGCTGGTGGGCATCGCC	1107
Qy	1018	AATTACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACT	1077
Db	1108	AACTACTACGCGCTGCTGCACCAGCAGAAGAGCCGCGCCTTCTACCGCATCCAGGCCACG	1167
Qy	1078	CGTATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAG	1137
Db	1168	CGGCTGATGACCGGCGCCGGAACGTGCTGCGCAGACACGCGGCGGACGCCTCGCGCAGG	1227
Qy	1138	GCCTCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTC	1197
Db	1228	GCGGC---GCCGGCCGAGGGCGCGGGCGAGGACGAAGACGACGGCGCCAGCCGCATCTTC	1284
Qy	1198	TTTGACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTG	1257
Db	1285	TTCGAGCCTAGCCTCTACCACTGCCTGGAGAACTGCGGCTCCGTGCTGCTGTCCGTCAG	1344
Qy	1258	AGGAAAGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCT	1317
Db	1345	TGCCAGGGCGGCGAGGGCAACAGCACCTTCTACGTGGACTACCGCACTGAGGACGGCTCT	1404
Qy	1318	GCCAATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAG	1377
Db	1405	GCCAAGGCGGGCTCCGACTACGAGTACAGCGAGGGCACGCTGGTGTCAAACCAGGCGAG	1464
Qy	1378	ACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACAC	1437
Db	1465	ACGCAGAAGGAGCTGCGCATCGGCATCATCGACGACGACATCTTCGAGGAGGACGAGCAT	1524
Qy	1438	TTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCT	1497
Db	1525	TTCTTCGTGCGGCTGCTGAACCTGCGCGTGGGCGACGCGCAGGGCATGTTGAGCCG---	1581
Qy	1498	CCAGCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCC	1557
Db	1582	-----GACGGCGGCGGGCGGCCCAAGGGCGGCTGGTGGCGCCGCTGCTGGCC	1629
Qy	1558	ACAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATT	1617

Db	1630	ACCGTCACCATCCTGGACGACGACCACGCAGGCATCTTCTCCTTCCAGGACCGCCTGCTG	1689
Qy	1618	CATGTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGG	1677
Db	1690	CACGTGAGCGAGTGCATGGGCACCGTGGACGTGCGCGTCGTGCGCAGCTCGGGCGCGCGC	1749
Qy	1678	GGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGAC	1737
Db	1750	GGCACCGTGCGCCTTCCCTACCGCACGGTGGACGGCACGGCGCGCGGCGGGCGGCGTGCAC	1809
Qy	1738	TTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGG	1797
Db	1810	TACGAGGACGCGTGCGGAGAGCTGGAGTTTGGCGACGACGAGACCATGAAAACCTCTTCAG	1869
Qy	1798	GTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGT	1857
Db	1870	GTGAAGATAGTTGATGACGAGGAATATGAGAAAAAGGATAATTTCTTCATTGAGCTGGGC	1929
Qy	1858	GAACCGAAATGGATGGAACGTGGAATATCAGATGTGACA-----GAC	1899
Db	1930	CAGCCCCAGTGGCTTAAGCGAGGGATTTAGCTCTGCTACTCAATCAAGGGGATGGGGAC	1989
Qy	1900	AGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTA	1959
Db	1990	AGGAAGCTAACAGCCGAGGAGGAGGAGGCTCGGAGGATAGCAGAGATGGGCAAGCCAGTT	2049
Qy	1960	TTGGGTGAACACCCCAAAGTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACG	2019
Db	2050	CTTGGGGAGAACTGCCGGCTGGAGGTCATCATCGAGGAGTCATATGATTTTAAGAACACG	2109
Qy	2020	GTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGTTGTGGGGACCCATTCTGGAGG	2079
Db	2110	GTGGATAAACTCATCAAGAAAACGAACCTTGGCCTTGTAATTGGGACCCATTTCATGGAGG	2169
Qy	2080	GACCAGTTCATGGAGGCCATCACCGTCAGTGCAGC---AGGGGATGAGGATGAGGATGAA	2136
Db	2170	GAGCAGTTTTTTAGAGGCAATTACGGTGAGCGCAGGGGACGAGGAGGAGGAGGACGGG	2229
Qy	2137	TCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTC	2196
Db	2230	TCCCGGGAGGAGCGGCTGCCGTCGTGCTTTGACTACGTGATGCACTTCCTGACGGTGTTC	2289
Qy	2197	TGGAAGGTGCTGTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTC	2256
Db	2290	TGGAAGGTGCTCTTCGCCTGTGTGCCCCCACCAGTACTGCCACGGCTGGGCCTGCTTT	2349
Qy	2257	GCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCAC	2316
Db	2350	GGTGTCTCCATCCTGGTCATCGGCCTGCTCACCGCCCTCATTGGGGACCTCGCCTCCAC	2409
Qy	2317	TTCGGCTGCACCATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTCGTGGCATTGGC	2376
Db	2410	TTCGGCTGCACCGTTGGCCTCAAGGACTCTGTCAATGCTGTGTCTTCGTTGCCCTGGGC	2469
Qy	2377	ACCTCTGTCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGAC	2436
Db	2470	ACCTCCATCCCTGACACGTTTCGCCAGCAAGGTGGCGGCGCTGCAGGACCAAGTGCGCCGAC	2529

Qy 141 CTGTTCAAGGGTCATCGGACTGCAAGGAGGGTGTCATCTGCCAATCTGGTACCCGGAGAA 200
||| ||| || | |||| | || || | |||| | || | || |
Db 126 CTGCCAAGGTTCTACCGCTGCCAACCAGGGGTGCTGCTGCCTGTGTGGGAACCCGACGA 185

Qy	201	CCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCATTTTTGTGGCCCTGATATACAT	260
Db	186	CCCATCACTGGGGGACAAGGCTGCACGGGCCGTGGTGTACTTTGTGGCCATGGTCTACAT	245
Qy	261	GTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTC	320
Db	246	GTTCTTGGGTCTGTCTATCATTGCTGATCGTTTTATGGCATCCATTGAGGTCATCACATC	305
Qy	321	TCAAGAGAGGGAGGTGACAATTAAGAAACCAATGGAGAAACCAGCACAAACCACTATTTCG	380
Db	306	CAAGGAGAAAGAGATCACCATCACCAAGGCAAATGGGGAGACCAGCGTGGGCACTGTACG	365
Qy	381	GGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGA	440
Db	366	CATCTGGAATGAAACGGTGTCCAACCTTACACTCATGGCCCTGGGCTCCTCAGCACCTGA	425
Qy	441	GATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCAATTGCTGGTGATCTGGGACC	500
Db	426	GATTCTGCTGTCTGTCTATCGAGGTCTGTGGCCACAACCTCCAGGCGGGTGAGCTAGGCC	485
Qy	501	TTCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTA	560
Db	486	AGGCACCATCGTGGGCAGTGCCGCCTTCAACATGTTTGTGGTCATTGCTGTGTGTGTGTA	545
Qy	561	CGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGC	620
Db	546	TGTCATCCCGGCTGGTGAGAGCCGTAAGATCAAGCACTTAAGGGTCTTCTTCGTCACAGC	605
Qy	621	TGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGG	680
Db	606	CTCTTGGAGCATCTTTGCCTATGTCTGGCTTTATCTCATTCTAGCAGTTTTCTCTCCAGG	665
Qy	681	TGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGCTCTTCT	740
Db	666	CGTGGTCCAGGTGTGGGAGGCACTGCTCACGCTGGTCTTCTTCCCGGTGTGTGTGGTGT	725
Qy	741	GGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCAC	800
Db	726	CGCCTGGATGGCGGACAAGCGACTGCTCTTCTACAAGTACGTGTACAAGCGCTATCGCAC	785
Qy	801	AGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGAT	860
Db	786	CGACCCTCGCAGCGGAATCATCATCGGGGAGAGGGAGACCCGCCAAGAGCATCGAGCT	845
Qy	861	GGATGGGAAAATGATGAATTCCCATTTCTAGATGGGAA-----CCTGGTGCC	908
Db	846	GGATGGCACATTTCGTGGGCACTGAGGTCCCAGGCGAGCTGGGTGCATTGGGCACAGGTCC	905
Qy	909	CCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCT	968
Db	906	CGCTGAGGCGCGTGAGCTGGACGCCAGCCGGCGGAGGTCATCCAGATTCTTAAGGACTT	965
Qy	969	GAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGC	1028
Db	966	AAAGCAGAAGCACCCGGATAAGGACCTGGAGCAGCTGGTGGGCATCGCCAAGTACTATGC	1025

Qy 1029 TCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGAC 1088
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Db 1026 ACTGCTGCACCAGCAGAAGAGCCGTGCCTTCTACCGCATCCAGGCCACGCGGCTGATGAC 1085

Qy 1089 TGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCAT 1148
 ||||| ||||| | ||| ||| ||| ||| ||| ||| |||

Db 1086 AGGTGCGGGCAACGTGCTGCGCCGACACGCTGCGGATGCTGCCCCGAGG---CCTGGGGC 1142

Qy 1149 GAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATG 1208
 | ||| | | ||||| || || | | ||||| || |

Db 1143 CAACGATGGTGCCCCGATGATGAGGACGATGGTGCCAGCCGCATCTTCTTTGAGCCCAG 1202

Qy 1209 TTCTTACCACTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGG 1268
 ||||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1203 CCTCTACCACTGCCTGGAGAAGTGTGGGGTCACTGCTGCTGCTGCGGTGGCTTGCCAGGGTGG 1262

Qy 1269 AGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGG 1328
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Db 1263 TGAGGGCAACAGCACCTTCTACGTGGATTACCGCACGGAGGATGGCTCTGCAAAGGCAGG 1322

Qy 1329 GGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGA 1388
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Db 1323 CTCCGATTATGAGTACAGCGAGGGGCACGCTGGTGTTCAGCCCGGGGAGACGCAGAAGGA 1382

Qy 1389 GTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAG 1448
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Db 1383 GCTGCGCATCGGCATCATCGACGACGACATCTTCGAGGAGGACGAGCACTTCTTCGTGAG 1442

Qy 1449 GTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATT 1508
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Db 1443 GCTGCTGAACCTGCGTGTGGGCGATGCTCAGGGCATGTTGAG-----CC 1487

Qy 1509 CAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACAGTTACCAT 1568
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Db 1488 CGACGGCGGTGGGCGGCCAAGGGGCGGCTGGTGGCGCCACTGCTGGCCACCGTCACCAT 1547

Qy 1569 CTTGGATGATGACCATGCAGGCATCTTCACTTTGAATGTGATACTATTATGTCAGTGA 1628
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Db 1548 TCTGGACGACGACCACGCGGGCATCTTCTCCTTCCAGGACCGCCTGCTGCATGTGAGCGA 1607

Qy 1629 GAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCAT 1688
 | | || | ||||| || || |||| | || | || | || |

Db 1608 GTGCATGGGCACCGTGGATGTGCGTGTGGTGCAGCTCTGGCGCACGTGGCACCGTACG 1667

Qy 1689 CGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACAC 1748
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Db 1668 CCTTCCCTACCGCACAGTGGACGGCACGGCTCGTGGTGGTGGTGTGCACTACGAGGATGC 1727

Qy 1749 ATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGT 1808
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Db 1728 TTGTGGAGAGCTGGAGTTCGGCGATGACGAGACCATGAAGACTCTTCAGGTCAAGATAGT 1787

Qy 1809 AGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATG 1868
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Db 1788 GGACGACGAAGAGTATGAGAAGAAGGACAACCTTCTTCATCGAGCTGGGCCAGCCCCAGTG 1847

Qy 1869 GATGGAACGTGGAATATCAGATGTGAC-----AGACAGGAAGCTGAC 1910

Db	1848	GCTTAAGCGGGGCATCTCAGCTCTGCTACTCAACCAAGGGGATGGAGACAGGAAGCTGAC	1907
Qy	1911	TATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACA	1970
Db	1908	TGCAGAGGAGGAGGAGGCCAGAGGATAGCAGAGATGGGCAAGCCAGTTCTTGGGGAGAA	1967
Qy	1971	CCCCAACTAGAAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAACT	2030
Db	1968	CTGTGCGCTCGAGGTCATCATCGAGGAGTCTTATGACTTTAAGAATACGGTGGATAAACT	2027
Qy	2031	GATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCAT	2090
Db	2028	CATAAAGAAAACAAACCTGGCCTTGGTGATTGGGACCCACTCATGGAGGGAGCAGTTTTT	2087
Qy	2091	GGAGGCCATCACCGTCAGTGCAGCA---GGGGATGAGGATGAGGATGAATCCGGGGAGGA	2147
Db	2088	AGAGGCAGTTACAGTGAGCGCAGGGGACGAGGAGGAGGATGAGGATGGGTCTCGTGAGGA	2147
Qy	2148	GAGGCTGCCCTCCTGCTTTGACTACGTGATGCACCTCCTGACTGTCTTCTGGAAGGTGCT	2207
Db	2148	GCGGCTGCCATCCTGCTTTGACTACGTGATGCACCTCCTGACGGTGTTCTGGAAAGTTCT	2207
Qy	2208	GTTTGCCTGTGTGCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCAT	2267
Db	2208	GTTCGCCTGCCTTCCACCCACGGAGTACTGCCATGGCTGGGCCTGCTTTGGTGTCTGCAT	2267
Qy	2268	CCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCAC	2327
Db	2268	CCTGGTCATTGGTCTGCTCACTGCCCTCATCGGAGACCTGGCCTCACACTTTGGGTGCAC	2327
Qy	2328	CATTGGTCTCAAAGATTCAAGTACAGCTGTTGTTTTCTGGGCATTTGGCACCTCTGTCCC	2387
Db	2328	CGTGGGCCTCAAGGACTCAGTCAACGCCGTGGTCTTCTGGGCTCTGGGCACCTCCATCCC	2387
Qy	2388	AGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGG	2447
Db	2388	TGACACGTTTGCCAGCAAAGGTGGCCGCGCTGCAGGACCAGTGCGCCGACGCGTCCATCGG	2447
Qy	2448	CAACGTGACGGGCAGCAACGCCGTCAATGTCTTCTGGGCATCGGCCTGGCCTGGTCCGT	2507
Db	2448	TAACGTGACCGGCTCCAATGCGGTGAACGTGTCTTCTGGGCCTGGGTGTGGCCTGGTCCGT	2507
Qy	2508	GGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTCCACGTGTCGGCCGGCACACTGGC	2567
Db	2508	GGCCGCAGTGTACTGGGCGGTGCAGGGTCGCCCTTCGAGGTGCGTACAGGCACGCTGGC	2567
Qy	2568	CTTCTCCGTCACCCCTCTTACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGACCG	2627
Db	2568	CTTCTCGGTCACACTGTTTACCCTCTTCGCCTTCGTGGGCATCGCAGTGCTCTTGACCG	2627
Qy	2628	AAGGCGGCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAAC	2687
Db	2628	GCGCCGGCCACACATCGGCGGCGAGCTGGGCGGCCCCGCGGGGACCCAAGCTAGCCACCAC	2687
Qy	2688	ATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTG	2747

Db 2688 CGCTCTCTTCCTGGGCCTCTGGTTCCTCTACATTCTCTTCGCCAGCCTGGAGGCTTATTG 2747

Qy 2748 CTACATCAAGGGGTTCTA 2765
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Db 2748 CCACATTCGGGGCTTCTA 2765

RESULT 15

US-09-901-419-1

; Sequence 1, Application US/09901419
 ; Patent No. US20020069421A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Curators of the University of Missouri
 ; TITLE OF INVENTION: LARGE SCALE EXPRESSION AND PURIFICATION OF RECOMBINANT
 ; TITLE OF INVENTION: PROTEINS
 ; FILE REFERENCE: UMO1531.1
 ; CURRENT APPLICATION NUMBER: US/09/901,419
 ; CURRENT FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: 60/218,125
 ; PRIOR FILING DATE: 2000-01-13
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4087
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (268)..(3180)
 ; NAME/KEY: sig_peptide
 ; LOCATION: (268)..(363)
 ; NAME/KEY: misc_feature
 ; LOCATION: (3178)
 ; OTHER INFORMATION: A Poly (H) affinity tag comprising 6 His residues
 ; OTHER INFORMATION: have been inserted at the C-Terminus end of the
 ; OTHER INFORMATION: coding region of the protein

US-09-901-419-1

Query Match 44.4%; Score 1227.8; DB 9; Length 4087;
 Best Local Similarity 67.1%; Pred. No. 0;
 Matches 1935; Conservative 0; Mismatches 777; Indels 171; Gaps 7;

Qy 46 TTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCA 105
 | | | | | | | | | | | | | | | | | | | |

Db 307 TTTCACGTGATAGCCATGGTGGCTCTCTGTTTTCCCATGTGGACCATATAAGTGCTGAG 366

Qy 106 GGGGACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAG 165
 | | | | | | | | | | | | | | | | | | | |

Db 367 ACAGAAATGGAAGGAGAAGGCAACGAGACTGGCGAGTGTACTGGCTCCTATTACTGTAAG 426

Qy 166 GAGGGTGTTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCC 225
 | | | | | | | | | | | | | | | | | | | |

Db 427 AAGGGGGTGATTTTACCCATTTGGGAGCCCCAGGACCCTTCCTTTGGAGACAAAATTGCT 486

Qy 226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCT 285
 | | | | | | | | | | | | | | | | | | | |

Db 487 AGAGCGACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCAATCATTGCT 546

Qy	286	GACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAG	345
Db	547	GACCGGTTTCATGTCTCTATAGAAGTCATCACGTCTCAAGAGAAAGAAATCACCATAAAG	606
Qy	346	AAACCCAATGGAGAAACCAGCACAACCACTATTCTGGGTCTGGAATGAAACTGTCTCCAAC	405
Db	607	AAACCCAATGGAGAGACCACCAAGACAACCTGTGAGGATCTGGAATGAGACAGTGTCCAAC	666
Qy	406	CTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTG	465
Db	667	CTGACCTTGATGGCCCTGGGTTCTTCAGCTCCAGAGATTCTCCTTTCAGTAATCGAGGTG	726
Qy	466	TGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGAGGCC	525
Db	727	TGTGGCCATAACTTCACTGCAGGAGACCTTGGCCCTAGCACCATCGTGGGGAGTGCTGCA	786
Qy	526	TTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGC	585
Db	787	TTCAACATGTTTCATCATCATTGCCCTTTGTGTGTATGTCGTCCCGGATGGGGAGACAAGG	846
Qy	586	AAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATC	645
Db	847	AAGATCAAGCATCTGCGTGTGTTCTTTGTGACAGCAGCATGGAGCATCTTTGCCTATACC	906
Qy	646	TGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTC	705
Db	907	TGGCTTTACATCATTTTGTCTGTGTCAGCTCCCCTGGGGTCGTGGAGGTCTGGGAAGGTTTG	966
Qy	706	CTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTG	765
Db	967	CTTACTTTCTTCTTCTTCCCCATCTGCGTTGTGTTTGCTTGGGTGGCAGACAGGAGGCTT	1026
Qy	766	CTCTTCTACAAATACATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATA	825
Db	1027	CTGTTTTTACAAGTATGTCTACAAGAGGTATCGGGCTGGCAAGCAGAGGGGAATGATTATT	1086
Qy	826	GAGACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATG	876
Db	1087	GAACACGAAGGAGACAGGCCATCTTCCAAGACAGAAATTGAAATGGATGGGAAAGTGGTC	1146
Qy	877	AATTCCCATTTC-----TAGATGGGAACCTGGTGCCCTGGAAGGGAAG-----	921
Db	1147	AATTCCCATGTTGACAGTTTCTTAGATGGAGCCCTGGTTCTGGAGGTTGATGAGAGGGAC	1206
Qy	922	---GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAA	978
Db	1207	CAAGATGATGAAGAAGCCAGGCGAGAAATGGCTAGGATTCTGAAGGAACCTCAAGCAGAAG	1266
Qy	979	CACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCAC	1038
Db	1267	CATCCAGAGAAGGAAATAGAGCAATTAATAGAATTAGCCAATTACCAAGTCTTAAGTCAG	1326
Qy	1039	CAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGC	1098
Db	1327	CAGCAAAAAGTCGAGCGTTTTACCGTATTCAAGCTACCCGCTGATGACCGGAGCAGGC	1386

Qy	1099	AATATCCCTGAAGAAAACATGCAGCAGAACAAGCCAAGAAGGCCCTCCAGCATGAGCGAGGTG	1158
Db	1387		
	1387	AACATTTTAAAGAGGCATGCAGCAGACCAAGCCAGGAAAGCTGTCAGCATGCATGAGGTC	1446
Qy	1159	CACACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC	1215
Db	1447		
	1447	AACACGGAAGTGGCTGAAAATGACCCTGTCAGTAAGATCTTCTTTGAACAAGGGACATAT	1506
Qy	1216	CAGTGCCTGGGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATG	1275
Db	1507		
	1507	CAGTGTCTGGGAACTGTGGCACAGTAGCCCTGACCATTATCCGCAGAGGTGGTGATTTG	1566
Qy	1276	TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCGCCAATGCAGGGGCTGAC	1335
Db	1567		
	1567	ACCAACACTGTGTTTGTTGACTTCAGAACAGAGGATGGCACAGCCAATGCTGGATCTGAT	1626
Qy	1336	TATGAGTTCACAGAGGGCACGGTGGTTCGAAGCCAGGAGAGACCCAGAAGGAGTTCCTC	1395
Db	1627		
	1627	TACGAATTTACCGAAGGAACGTGGTCTTTAAGCCTGGTGAGACCCAGAAGGAAATCAGA	1686
Qy	1396	GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC	1455
Db	1687		
	1687	GTTGGCATCATTGATGATGACATCTTTGAGGAGGATGAGAATTTCTTGTGCATCTCAGC	1746
Qy	1456	AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT	1515
Db	1747		
	1747	AACGTCAAAGTATCTTTGGAAGCCTCGGAAGACGGCATCTGGAAGC-----CAGT	1797
Qy	1516	CTTCCCTTGCCCTCGGGCTGTCCCTAGCCTCCCCCTGTGTGGCCACAGTTACCATCTTGGAT	1575
Db	1798		
	1798	CATGTCTCTACCCCTTGCTTGCCTGGGATCCCCCTCCACTGCCACCGTGACTATTTTGTAT	1857
Qy	1576	GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTATGTCAGTGAGAGTATT	1635
Db	1858		
	1858	GATGACCATGCTGGCATCTTTACTTTTGAGGAACCGGTGACTCATGTGAGTGAGAGCATT	1917
Qy	1636	GGTGTATGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCC	1695
Db	1918		
	1918	GGCATCATGGAGGTGAAAGTTCTGAGAACATCTGGAGCACGTGGAAATGTTATCGTTCCC	1977
Qy	1696	TTTAGGACAGTAGAAGGGACAGCCAAGGTTGGCGGTGAGGACTTTGAAGACACATATGGG	1755
Db	1978		
	1978	TATAAGACCATTGAGGGGACCGCCAGAGGTGGAGGGGAGGACTTTGAGGACACATGCGGA	2037
Qy	1756	GAGTTGGAATTCAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAG	1815
Db	2038		
	2038	GAGCTCGAGTTCAGAAATGACGAAATGTCAAACAATATCAGTCAAGGTAATTGATGAT	2097
Qy	1816	GAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGG--	1873
Db	2098		
	2098	GAGGAGTATGAGAAAAACAAGACCTTCTTCCTTGAGATTGGAGAGCCCCGCCFGGTGGAG	2157
Qy	1874	-----AACGTGGAA	1882
Db	2158		
	2158	ATGAGTGAGAAGAAAGCCCTGTTATTGAATGAGCTTGGTGGCTTCACAATAACAGGGAAA	2217
Qy	1883	TATCAGATGTGACAGACAG-----	1901

Db	2218	TACCTGTATGGCCAGCCTGTCTTCAGGAAAGTTCATGCTAGAGAACATCCACTCCCCTCT	2277
Qy	1902	-----GAAGCTGACTATGGAAGAAGAG	1923
Db	2278	ACTATAATCACCATCGCAGATGAATATGATGACAAGCAGCCACTGACCAGCAAAGAGGAG	2337
Qy	1924	GAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAAGTAGAA	1983
Db	2338	GAAGAGAGGCGCATTGCGGAAATGGGGCGCCCCATTCTGGGAGAGCACACCAGACTGGAG	2397
Qy	1984	GTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACA	2043
Db	2398	GTGATCATTGAAGAATCCTACGAGTTCAAGAGTACCGTGGACAAACTGATTAAGAAGACA	2457
Qy	2044	AACCTGGCCTTGGTTGTGGGGACCCATTCTGGAGGGACCAGTTCATGGAGGCCATCACC	2103
Db	2458	AACCTAGCCCTCGTGGTTGGGACGAACAGCTGGAGAGAGCAGTTCATCGAGGCGATCACT	2517
Qy	2104	GTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGC	2163
Db	2518	GTCAGTGCTGGGAAGATGACGATGACGACGAATGTGGGGAGGAGAAGCTGCCCTCCTGT	2577
Qy	2164	TTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCC	2223
Db	2578	TTTGACTACGTGATGCACTTTCTGACTGTGTTCTGGAAGGTCTCTTCGCCTTTGTCCCC	2637
Qy	2224	CCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATG	2283
Db	2638	CCGACAGAGTACTGGAACGGCTGGGCGTGTTTCATCGTCTCCATCCTCATGATCGGCCTA	2697
Qy	2284	CTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGAT	2343
Db	2698	CTGACGGCTTTTCATTGGAGACCTCGCTTCCCACTTCGCCTGCACCATCGCCCTGAAGGAT	2757
Qy	2344	TCAGTCACAGCTGTTGTTTTCTGGGCATTTGGCACCTCTGTCCCAGATACGTTTGCCAGC	2403
Db	2758	TCCGTGACCGCGGTGGTGTTCGTTGCGCTTGAACCTCAGTGCCAGACACATTTGCAAGC	2817
Qy	2404	AAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGC	2463
Db	2818	AAAGTGGCCGCCACCCAGGACCAGTATGCGGATGCATCCATAGGTAACGTACAGGCAGC	2877
Qy	2464	AACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGG	2523
Db	2878	AACGCGGTGAACGTCTTCCTGGGCATCGGTGTGGCCTGGTCCATCGCCGCCATCTACCAC	2937
Qy	2524	GCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCAACCTC	2583
Db	2938	GCGGCCAACGGGAACAGTTCAAAGTGTCCTGGCACGCTAGCTTTTTCTGTCACTCTC	2997
Qy	2584	TTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTAACGAAGGCGGCCGCACCTG	2643
Db	2998	TTCACCATTTTTGCTTTTCATCAATGTGGGGGTGCTGCTGTATCGGCGGAGGCCAGAAATT	3057
Qy	2644	GGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGC	2703

Db 3058 GGAGGTGAGCTGGGTGGGCCCCGGACTGCCAAGCTCCTCACATCCTGCCTCTTTGTGCTC 3117
 Qy 2704 CTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTT 2763
 ||||| | |||| | || | | ||||| || | || | ||
 Db 3118 CTGTGGCTCTTGTACATTTCTTCTCCTCCCTGGAGGCCTACTGCCACATAAAAGGCTTC 3177
 Qy 2764 TAA 2766
 |||
 Db 3178 TAA 3180

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